

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Chen, Ruoping  
Dang, Huong T.  
5 Liaw, Chen W.  
Lin, I-Lin

(ii) TITLE OF INVENTION: Human Orphan G Protein-Coupled Receptors

(iii) NUMBER OF SEQUENCES: 74

10 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Arena Pharmaceuticals, Inc.  
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(C) CITY: San Diego  
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15 (E) COUNTRY: USA  
(F) ZIP: 92121

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
20 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
25 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Burgoon, Richard P.  
(B) REGISTRATION NUMBER: 34,787

(ix) TELECOMMUNICATION INFORMATION:

30 (A) TELEPHONE: (858) 453-7200  
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## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

40 ATGGTCTTCT CGGCAGTGTT GACTGCGTTC CATAACGGGA CATCCAACAC AACATTGTC 60

GTGTATGAAA ACACCTACAT GAATATTACA CTCCCTCCAC CATTCCAGCA TCCTGACCTC 120  
AGTCCATTGC TTAGATATAG TTTGAAACC ATGGCTCCC CTGGTTGAG TTCCTTGACC 180  
GTGAATAGTA CAGCTGTGCC CACAACACCA GCAGCATTTA AGAGCCTAAA CTTGCCTCTT 240  
CAGATCACCC TTTCTGCTAT AATGATATTTC ATTCTGTTG TGTCTTTCT TGGGAACTTG 300  
5 GTTGTGGCC TCATGGTTA CCAAAAAGCT GCCATGAGGT CTGCAATTAA CATCCTCCTT 360  
GCCAGCCTAG CTTTGCGAGA CATGTTGCTT GCAGTGCTGA ACATGCCCTT TGCCCTGGTA 420  
ACTATTCTTA CTACCCGATG GATTTTGAGG AAATTCTTCT GTAGGGTATC TGCTATGTTT 480  
TTCTGGTTAT TTGTGATAGA AGGAGTAGCC ATCCTGCTCA TCATTAGCAT AGATAGGTT 540  
CTTATTATAG TCCAGAGGCA GGATAAGCTA AACCCATATA GAGCTAAGGT TCTGATTGCA 600  
10 GTTCTTGGG CAACTTCCTT TTGTGTAGCT TTTCCTTAG CGCTAGGAAA CCCCGACCTG 660  
CAGATAACCTT CCCGAGCTCC CCAGTGTGTG TTTGGGTACA CAACCAATCC AGGCTACCAG 720  
GCTTATGTGA TTTTGATTTC TCTCATTCTT TTCTTCATAC CCTTCCTGGT AATACTGTAC 780  
TCATTTATGG GCATACTCAA CACCCTTCGG CACAATGCCT TGAGGATCCA TAGCTACCCT 840  
GAAGGTATAT GCCTCAGCCA GGCCAGCAA CTGGGTCTCA TGAGTCTGCA GAGACCTTTC 900  
15 CAGATGAGCA TTGACATGGG CTTTAAAACA CGTGCCTTCA CCACTATTTT GATTCTCTTT 960  
GCTGTCTTCA TTGTCTGCTG GGCCCCATTTC ACCACTTACA GCCTTGTGGC  
AACATTCAAGT1020  
AAGCACTTT ACTATCAGCA CAACTTTTTT GAGATTAGCA CCTGGCTACT GTGGCTCTGC1080  
TACCTCAAGT CTGCATTGAA TCCGCTGATC TACTACTGGA GGATTAAGAA ATTCCATGAT1140  
20 GCTTGCCTGG ACATGATGCC TAAGTCCTTC AAGTTTTGC CGCAGCTCCC TGGTCACACA1200  
AAGCGACGGA TACGTCTTAG TGCTGTCTAT GTGTGTGGGG AACATCGGAC GGTGGTGTGA1260

## (3) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 419 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30 Met Val Phe Ser Ala Val Leu Thr Ala Phe His Thr Gly Thr Ser Asn  
1 5 10 15

Thr Thr Phe Val Val Tyr Glu Asn Thr Tyr Met Asn Ile Thr Leu Pro  
20 25 30

Pro Pro Phe Gln His Pro Asp Leu Ser Pro Leu Leu Arg Tyr Ser Phe  
35 40 45

5 Glu Thr Met Ala Pro Thr Gly Leu Ser Ser Leu Thr Val Asn Ser Thr  
50 55 60

Ala Val Pro Thr Thr Pro Ala Ala Phe Lys Ser Leu Asn Leu Pro Leu  
65 70 75 80

Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu Phe Val Ser Phe  
10 85 90 95

Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln Lys Ala Ala Met  
100 105 110

Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala Phe Ala Asp Met  
115 120 125

15 Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val Thr Ile Leu Thr  
130 135 140

Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val Ser Ala Met Phe  
145 150 155 160

Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu Leu Ile Ile Ser  
20 165 170 175

Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp Lys Leu Asn Pro  
180 185 190

Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala Thr Ser Phe Cys  
195 200 205

25 Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu Gln Ile Pro Ser  
210 215 220

Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn Pro Gly Tyr Gln  
225 230 235 240

Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe Ile Pro Phe Leu  
30 245 250 255

Val Ile Leu Tyr Ser Phe Met Gly Ile Leu Asn Thr Leu Arg His Asn  
260 265 270

Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala  
275 280 285

35 Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile  
290 295 300

Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe

305                    310                    315                    320  
Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val  
                      325                        330                        335  
Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile  
5                        340                        345                        350  
Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro  
                      355                        360                        365  
Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp  
                      370                        375                        380  
10                    Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr  
                      385                        390                        395                        400  
Lys Arg Arg Ile Arg Pro Ser Ala Val Tyr Val Cys Gly Glu His Arg  
                      405                        410                        415  
Thr Val Val  
15

## (4) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1119 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
  
(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGTTAGCCA ACAGCTCCTC AACCAACAGT TCTGTTCTCC CGTGTCTGA CTACCGACCT 60  
25 ACCCACCGCC TGCACTTGGT GGTCTACAGC TTGGTGCTGG CTGCCGGGCT CCCCCCTAAC 120  
GGGCTAGCCC TCTGGGTCTT CCTGCGCGCG CTGCGCGTGC ACTCGGTGGT GAGCGTGTAC 180  
ATGTGTAACC TGGCGGCCAG CGACCTGCTC TTCACCCCTCT CGCTGCCCGT TCGTCTCTCC 240  
TACTACGCAC TGCACCACTG GCCCTTCCCC GACCTCCTGT GCCAGACGAC GGGCGCCATC 300  
TTCCAGATGA ACATGTACGG CAGCTGCATC TTCTGATGC TCATCAACGT GGACCGCTAC 360  
30 GCCGCCATCG TGCACCCGCT GCGACTGCGC CACCTGCGC GGCCCCGCGT GGCGCGCTG 420  
CTCTGCCTGG GCGTGTGGC GCTCATCCTG GTGTTGCCG TGCCCGCCGC CCGCGTGCAC 480  
AGGCCCTCGC GTTGCGCTA CCGGGACCTC GAGGTGCGCC TATGCTTCGA GAGCTTCAGC 540  
GACGAGCTGT GGAAAGGCAG GCTGCTGCC CTCGTGCTGC TGGCCGAGGC GCTGGGCTTC 600

CTGCTGCCCC TGGCGGCCGT GGTCTACTCG TCGGGCCGAG TCTTCTGGAC GCTGGCGCGC 660  
CCCGACGCCA CGCAGAGCCA GCGCGGCCGG AAGACCGTGC GCCTCCTGCT GGCTAACCTC 720  
GTCATCTTCC TGCTGTGCTT CGTGCCCTAC AACAGCACGC TGGCGGTCTA CGGGCTGCTG 780  
CGGAGCAAGC TGGTGGCGGC CAGCGTGCCT GCCCCGCGATC GCGTGCACGG GGTGCTGATG 840  
5 GTGATGGTGC TGCTGGCCGG CGCCAACTGC GTGCTGGACC CGCTGGTGTA CTACTTTAGC 900  
GCCGAGGGCT TCCGCAACAC CCTGCGCGC CTGGGCACTC CGCACCGGGC CAGGACCTCG 960  
GCCACCAACG GGACGCAGGC GGCCTCGCG CAATCCGAAA GGTCCGCCGT CACCACCGAC1020  
GCCACCAGGC CGGATGCCGC CAGTCAGGGG CTGCTCCGAC CCTCCGACTC CCACCTCTG1080  
TCTTCCTTCA CACAGTGTCC CCAGGATTCC GCCCTCTGA 1119

## 10 (5) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 372 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
15 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Ala Asn Ser Ser Ser Thr Asn Ser Ser Val Leu Pro Cys Pro  
1 5 10 15  
Asp Tyr Arg Pro Thr His Arg Leu His Leu Val Val Tyr Ser Leu Val  
20 20 25 30  
Leu Ala Ala Gly Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu  
35 35 40 45  
Arg Ala Leu Arg Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu  
25 50 55 60  
Ala Ala Ser Asp Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser  
65 65 70 75 80  
Tyr Tyr Ala Leu His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr  
85 85 90 95  
30 Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu  
100 100 105 110  
Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg  
115 120 125

Leu Arg His Leu Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly  
 130 135 140  
 Val Trp Ala Leu Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His  
 145 150 155 160  
 5 Arg Pro Ser Arg Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe  
 165 170 175  
 Glu Ser Phe Ser Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val  
 180 185 190  
 10 Leu Leu Ala Glu Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val  
 195 200 205  
 Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr  
 210 215 220  
 Gln Ser Gln Arg Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu  
 225 230 235 240  
 15 Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val  
 245 250 255  
 Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg  
 260 265 270  
 20 Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala  
 275 280 285  
 Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe  
 290 295 300  
 Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser  
 305 310 315 320  
 25 Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala  
 325 330 335  
 Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu  
 340 345 350  
 30 Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln  
 355 360 365  
 Asp Ser Ala Leu  
 370

## (6) INFORMATION FOR SEQ ID NO:5:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCCAACCTTCCAGGCT GAACGCCCTCA GAAGTCGCAG GCTCGTTGGG GTTGATCCTG 60  
GCAGCTGTCTG TGGAGGTGGG GGCACTGCTG GGCAACGGCG CGCTGCTGGT CGTGGTCTG 120  
5 CGCACGCCGG GACTGCGCGA CGCGCTCTAC CTGGCGCACC TGTGCGTCGT GGACCTGCTG 180  
CGGCCGCCT CCATCATGCC GCTGGGCCTG CTGGCCGCAC CGCCGCCCGG GCTGGGCCGC 240  
GTGCGCTGG GCCCGCGGCC ATGCCCGGCC GCTCGCTTCC TCTCCGCCGC TCTGCTGCCG 300  
GCCTGCACGC TCAGGGTGGC CGCACTTGGC CTGGCACGCT ACCGCCTCAT CGTGCACCCG 360  
CTGCGGCCAG GCTCGCGGCC GCCGCCTGTG CTCGTGCTCA CCGCCGTGTG GGCCGCCGG 420  
10 GGACTGCTGG GCGCGCTCTC CCTGCTCGGC CCGCCGCCCG CACCGCCCCC TGCTCCTGCT 480  
CGCTGCTCGG TCCTGGCTGG GGGCCTCGGG CCCTTCGGC CGCTCTGGC CCTGCTGCC 540  
TTCCGCGCTGC CCGCCCTCCT GCTGCTCGGC GCCTACGGCG GCATCTTCGT GGTGGCGCGT 600  
CGCGCTGCCCG TGAGGCCCCC ACGGCCGGCG CGCGGGTCCC GACTCCGCTC GGACTCTCTG 660  
GATAGCCGCC TTTCCATCTT GCCGCCGCTC CGGCCTCGCC TGCCCCGGGG CAAGGCCGCC 720  
15 CTGGCCCCAG CGCTGGCCGT GGGCAATTG GCAGCCTGCT GGCTGCCTTA TGGCTGCGCG 780  
TGCCTGGCGC CCGCAGCGCG GGGCGCGGAA GCCGAAGCGG CTGTCACCTG GGTCGCCTAC 840  
TCGGCCTTCG CGGCTCACCC CTTCTGTAC GGGCTGCTGC AGCGCCCCGT GCGCTTGGCA 900  
CTGGGCCGCC TCTCTGCCG TGCACTGCCT GGACCTGTGC GGGCCTGCAC TCCGCAAGCC 960  
TGGCACCCGC GGGCACTCTT GCAATGCCTC CAGAGACCC CAGAGGGCCC TGCCGTAGGC 1020  
20 CCTTCTGAGG CTCCAGAACCA GACCCCCGAG TTGGCAGGAG GGCAGGAGCCC CGCATACCAG 1080  
GGGCCACCTG AGAGTTCTCT CTCCTGA 1107

(7) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 368 amino acids  
25 (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Asn Ser Thr Gly Leu Asn Ala Ser Glu Val Ala Gly Ser Leu  
 1 5 10 15

Gly Leu Ile Leu Ala Ala Val Val Glu Val Gly Ala Leu Leu Gly Asn  
 20 25 30

5 Gly Ala Leu Leu Val Val Val Leu Arg Thr Pro Gly Leu Arg Asp Ala  
 35 40 45

Leu Tyr Leu Ala His Leu Cys Val Val Asp Leu Leu Ala Ala Ala Ser  
 50 55 60

10 Ile Met Pro Leu Gly Leu Leu Ala Ala Pro Pro Pro Gly Leu Gly Arg  
 65 70 75 80

Val Arg Leu Gly Pro Ala Pro Cys Arg Ala Ala Arg Phe Leu Ser Ala  
 85 90 95

Ala Leu Leu Pro Ala Cys Thr Leu Gly Val Ala Ala Leu Gly Leu Ala  
 100 105 110

15 Arg Tyr Arg Leu Ile Val His Pro Leu Arg Pro Gly Ser Arg Pro Pro  
 115 120 125

Pro Val Leu Val Leu Thr Ala Val Trp Ala Ala Ala Gly Leu Leu Gly  
 130 135 140

20 Ala Leu Ser Leu Leu Gly Pro Pro Pro Ala Pro Pro Pro Ala Pro Ala  
 145 150 155 160

Arg Cys Ser Val Leu Ala Gly Gly Leu Gly Pro Phe Arg Pro Leu Trp  
 165 170 175

Ala Leu Leu Ala Phe Ala Leu Pro Ala Leu Leu Leu Gly Ala Tyr  
 180 185 190

25 Gly Gly Ile Phe Val Val Ala Arg Arg Ala Ala Leu Arg Pro Pro Arg  
 195 200 205

Pro Ala Arg Gly Ser Arg Leu Arg Ser Asp Ser Leu Asp Ser Arg Leu  
 210 215 220

30 Ser Ile Leu Pro Pro Leu Arg Pro Arg Leu Pro Gly Gly Lys Ala Ala  
 225 230 235 240

Leu Ala Pro Ala Leu Ala Val Gly Gln Phe Ala Ala Cys Trp Leu Pro  
 245 250 255

Tyr Gly Cys Ala Cys Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu  
 260 265 270

35 Ala Ala Val Thr Trp Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe  
 275 280 285

Leu Tyr Gly Leu Leu Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu

290                    295                    300

Ser Arg Arg Ala Leu Pro Gly Pro Val Arg Ala Cys Thr Pro Gln Ala  
305                    310                    315                    320

5 Trp His Pro Arg Ala Leu Leu Gln Cys Leu Gln Arg Pro Pro Glu Gly  
                      325                    330                    335

Pro Ala Val Gly Pro Ser Glu Ala Pro Glu Gln Thr Pro Glu Leu Ala  
                      340                    345                    350

Gly Gly Arg Ser Pro Ala Tyr Gln Gly Pro Pro Glu Ser Ser Leu Ser  
                      355                    360                    365

10 (8) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGGAATCAT CTTTCTCATT TGGAGTGATC CTTGCTGTCC TGGCCTCCCT CATCATTGCT 60  
ACTAACACAC TAGTGGCTGT GGCTGTGCTG CTGTTGATCC ACAAGAAATGA TGGTGTCAAGT 120  
20 CTCTGCTTCA CCTTGAATCT GGCTGTGGCT GACACCTTGA TTGGTGTGGC CATCTCTGGC 180  
CTACTCACAG ACCAGCTCTC CAGCCCTTCT CGGCCACAC AGAAGACCCT GTGCAGCCTG 240  
CGGATGGCAT TTGTCACTTC CTCCGCAGCT GCCTCTGTCC TCACGGTCAT GCTGATCACC 300  
TTTGACAGGT ACCTTGCCAT CAAGCAGCCC TTCCGCTACT TGAAGATCAT GAGTGGGTTTC 360  
GTGGCCGGGG CCTGCATTGC CGGGCTGTGG TTAGTGTCTT ACCTCATTGG CTTCCTCCCCA 420  
25 CTCGGAATCC CCATGTTCCA GCAGACTGCC TACAAAGGGC AGTGCAGCTT CTTTGCTGTA 480  
TTTCACCCCTC ACTTCGTGCT GACCCTCTCC TGCCTGGCT TCTTCCCAGC CATGCTCCTC 540  
TTTGTCTTCT TCTACTGCGA CATGCTCAAG ATTGCCTCCA TGCACAGCCA GCAGATTGCA 600  
AAGATGGAAC ATGCAGGAGC CATGGCTGGA GGTTATCGAT CCCCACGGAC TCCCAGCGAC 660  
TTCAAAGCTC TCCGTACTGT GTCTGTTCTC ATTGGGAGCT TTGCTCTATC CTGGACCCCC 720  
30 TTCCTTATCA CTGGCATTGT GCAGGGTGGCC TGCCAGGAGT GTCACCTCTA CCTAGTGCTG 780  
GAACGGTACC TGTGGCTGCT CGGCCTGGC AACTCCCTGC TCAACCCACT CATCTATGCC 840

TATTGGCAGA AGGAGGTGCG ACTGCAGCTC TACCACATGG CCCTAGGAGT GAAGAAGGTG 900  
CTCACCTCAT TCCTCCTCTT TCTCTGGCC AGGAATTGTG GCCCAGAGAG GCCCAGGGAA 960  
AGTTCCCTGTC ACATCGTCAC TATCTCCAGC TCAGAGTTTG ATGGCTAA 1008

## (9) INFORMATION FOR SEQ ID NO:8:

- 5       (i) SEQUENCE CHARACTERISTICS:  
          (A) LENGTH: 335 amino acids  
          (B) TYPE: amino acid  
          (C) STRANDEDNESS:  
          (D) TOPOLOGY: not relevant

10      (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser  
1                   5                   10                   15

Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu  
15                20                25                   30

Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala  
35                40                   45

Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp  
50                55                   60

Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu  
20                65                70                75                80

Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ser Val Leu Thr Val  
85                90                   95

Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg  
25                100                105                   110

Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly  
115               120                   125

Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro  
130               135                   140

Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val  
30                145                150                155                160

Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro  
165               170                   175

Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala  
35                180                185                   190

Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met  
 195 200 205  
 Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu  
 210 215 220  
 5 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro  
 225 230 235 240  
 Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu  
 245 250 255  
 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser  
 10 260 265 270  
 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu  
 275 280 285  
 Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe  
 290 295 300  
 15 Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu  
 305 310 315 320  
 Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly  
 325 330 335

## (10) INFORMATION FOR SEQ ID NO:9:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1413 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGACACTA CCATGGAAGC TGACCTGGGT GCCACTGGCC ACAGGCCCG CACAGAGCTT 60  
 GATGATGAGG ACTCCTACCC CCAAGGTGGC TGGGACACGG TCTTCCTGGT GGCCCTGCTG 120  
 CTCCTTGGGC TGCCAGCCAA TGGGTTGATG GCGTGGCTGG CGGGCTCCCA GGCCCGGCAT 180  
 30 GGAGCTGGCA CGCGTCTGGC GCTGCTCCTG CTCAGCCTGG CCCTCTCTGA CTTCTTGTTC 240  
 CTGGCAGCAG CGGCCTTCCA GATCCTAGAG ATCCGGCATG GGGGACACTG GCCGCTGGGG 300  
 ACAGCTGCCT GCCGCTTCTA CTACTTCCTA TGGGGCGTGT CCTACTCCTC CGGCCTCTTC 360  
 CTGCTGGCCG CCCTCAGCCT CGACCGCTGC CTGCTGGCGC TGTGCCACA CTGGTACCCT 420  
 GGGCACCGCC CAGTCCGCCT GCCCCTCTGG GTCTGCGCCG GTGTCTGGGT GCTGGCCACA 480

CTCTTCAGCG TGCCCTGGCT GGTCTTCCCC GAGGCTGCCG TCTGGTGGTA CGACCTGGTC 540  
ATCTGCCTGG ACTTCTGGGA CAGCGAGGAG CTGTCGCTGA GGATGCTGGA GGTCTGGGG 600  
GGCTTCCTGC CTTTCCTCCT GCTGCTCGTC TGCCACGTGC TCACCCAGGC CACAGCCTGT 660  
CGCACCTGCC ACCGCCAACAA GCAGCCCGCA GCCTGCCGGG GCTTCGCCCG TGTGCCAGG 720  
5 ACCATTCTGT CAGCCTATGT GGTCTGAGG CTGCCCTACC AGCTGGCCA GCTGCTCTAC 780  
CTGGCCTTCC TGTGGGACGT CTACTCTGGC TACCTGCTCT GGGAGGCCCT GGTCTACTCC 840  
GACTACCTGA TCCTACTCAA CAGCTGCCTC AGCCCCTTCC TCTGCCTCAT GGCCAGTGCC 900  
GACCTCCGGA CCCTGCTGCG CTCCGTGCTC TCGTCCTTCG CGGCAGCTCT CTGCGAGGAG 960  
CGGCCGGGCA GCTTCACGCC CACTGAGCCA CAGACCCAGC TAGATTCTGA GGGTCCA1020  
10 CTGCCAGAGC CGATGGCAGA GGCCCAGTCA CAGATGGATC CTGTGGCCA GCCTCAGGTG1080  
AACCCCACAC TCCAGCCACG ATCGGATCCC ACAGCTCAGC CACAGCTGAA CCCTACGGCC1140  
CAGCCACAGT CGGATCCCAC AGCCCAGCCA CAGCTGAACC TCATGGCCA GCCACAGTCA1200  
GATTCTGTGG CCCAGCCACA GGCAAGACACT AACGTCCAGA CCCCTGCACC TGCTGCCAGT1260  
TCTGTGCCCA GTCCCTGTGA TGAAGCTTCC CCAACCCAT CCTCGCATCC TACCCAGGG1320  
15 GCCCTTGAGG ACCCAGCCAC ACCTCCTGCC TCTGAAGGAG AAAGCCCCAG CAGCACCCCG1380  
CCAGAGGCGG CCCCAGGCAG TGA 1413

## (11) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 468 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

25 Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro  
1 5 10 15  
Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp  
20 25 30  
Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly  
30 35 40 45  
Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr

	50	55	60	
	Arg Leu Ala Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe			
	65	70	75	80
	Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His			
5	85	90	95	
	Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly			
	100	105	110	
	Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp			
	115	120	125	
10	Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro			
	130	135	140	
	Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr			
	145	150	155	160
15	Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp			
	165	170	175	
	Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser			
	180	185	190	
	Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu			
	195	200	205	
20	Leu Val Cys His Val Leu Thr Gln Ala Thr Arg Thr Cys His Arg Gln			
	210	215	220	
	Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile			
	225	230	235	240
25	Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu			
	245	250	255	
	Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp			
	260	265	270	
	Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu			
	275	280	285	
30	Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu			
	290	295	300	
	Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro			
	305	310	315	320
35	Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly			
	325	330	335	
	Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro			
	340	345	350	

Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro  
355 360 365

Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro  
370 375 380

5 Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser  
385 390 395 400

Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala  
405 410 415

10 Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala Ser Pro Thr Pro Ser  
420 425 430

Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro Ala Thr Pro Pro Ala  
435 440 445

Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro Glu Ala Ala Pro Gly  
450 455 460

15 Ala Gly Pro Thr  
465

## (12) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1248 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

25 ATGTCAGGGA TGGAAAACT TCAGAACATGCT TCCTGGATCT ACCAGCAGAA ACTAGAACAT 60  
CCATTCCAGA AACACCTGAA CAGCACCGAG GAGTATCTGG CCTTCCTCTG CGGACCTCGG 120  
CGCAGCCACT TCTTCCTCCC CGTGTCTGTG GTGTATGTGC CAATTTTGTC GGTGGGGTC 180  
ATTGGCAATG TCCTGGTGTG CCTGGTGATT CTGCAGCACC AGGCTATGAA GACGCCACC 240  
AACTACTACC TCTTCAGCCT GGC GGCTCTCT GACCTCCTGG TCCTGCTCCT TGGAATGCC 300  
30 CTGGAGGTCT ATGAGATGTG GCGCAACTAC CCTTTCTTGT TCGGGCCCGT GGGCTGCTAC 360  
TTCAAGACGG CCCTCTTGA GACCGTGTGC TTCGCCTCCA TCCTCAGCAT CACCACCGTC 420  
AGCGTGGAGC GCTACGTGGC CATCCTACAC CCGTTCCGCG CCAAAGTGCA GAGCACCCGG 480  
CGCCGGGCCCT TCAGGATCCT CGGCATCGTC TGGGGCTTCT CCGTGCTCTT CTCCCTGCC 540

AACACCAGCA TCCATGGCAT CAAGTTCCAC TACTTCCCCA ATGGGTCCCT GGTCCCAGGT 600  
TCGGGCCACCT GTACGGTCAT CAAGCCCAGT TGGATCTACA ATTCATCAT CCAGGTCACC 660  
TCCTTCCTAT TCTACCTCCT CCCCATGACT GTCATCAGTG TCCTCTACTA CCTCATGGCA 720  
CTCAGACTAA AGAAAGACAA ATCTCTTGAG GCAGATGAAG GGAATGCAA AATTCAAAGA 780  
5 CCCTGCAGAA AATCAGTCAA CAAGATGCTG TTTGTCTTGG TCTTAGTGTT TGCTATCTGT 840  
TGGGCCCCGT TCCACATTGA CCGACTCTTC TTCAGCTTG TGGAGGAGTG GAGTGAATCC 900  
CTGGCTGCTG TGTTCAACCT CGTCCATGTG GTGTCAGGTG TCTTCTTCTA CCTGAGCTCA 960  
GCTGTCAACC CCATTATCTA TAACTACTG TCTGCCGCT TCCAGGCAGC ATTCCAGAAT1020  
GTGATCTCTT CTTTCCACAA ACAGTGGCAC TCCCAGCATG ACCCACAGTT GCCACCTGCC1080  
10 CAGCGGAACA TCTTCCTGAC AGAATGCCAC TTTGTGGAGC TGACCGAAGA TATAGGTCCC1140  
CAATTCCCAT GTCAGTCATC CATGCACAAAC TCTCACCTCC CAACAGCCCT CTCTAGTGAA1200  
CAGATGTCAA GAACAAACTA TCAAAGCTTC CACTTTAACAA AACCTGTA 1248

## (13) INFORMATION FOR SEQ ID NO:12:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 415 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: not relevant

## (ii) MOLECULE TYPE: protein

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln  
1 5 10 15  
Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr  
20 25 30  
25 Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val  
35 40 45  
Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val  
50 55 60  
30 Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr  
65 70 75 80  
Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu  
85 90 95

Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe  
100 105 110

Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr  
115 120 125

5 Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg  
130 135 140

Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg  
145 150 155 160

10 Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu  
165 170 175

Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe  
180 185 190

Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys  
195 200 205

15 Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe  
210 215 220

Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala  
225 230 235 240

20 Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala  
245 250 255

Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val  
260 265 270

Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg  
275 280 285

25 Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val  
290 295 300

Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser  
305 310 315 320

30 Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala  
325 330 335

Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln  
340 345 350

His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu  
355 360 365

35 Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys  
370 375 380

Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu  
385 390 395 400

Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr  
405 410 415

## (14) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGCCAGATA CTAATAGCAC AATCAATTAA TCACTAAGCA CTCGTGTTAC TTTAGCATTT 60  
TTTATGTCCT TAGTAGCTTT TGCTATAATG CTAGGAAATG CTTTGGTCAT TTTAGCTTTT 120  
GTGGTGGACA AAAACCTTAG ACATCGAAGT AGTTATTTTT TTCTTAACCTT GGCCATCTCT 180  
GACTTCTTTG TGGGTGTGAT CTCCATTCTT TTGTACATCC CTCACACGCT GTTCGAATGG 240  
15 GATTTTGAA AGGAAATCTG TGTATTTGG CTCACTACTG ACTATCTGTT ATGTACAGCA 300  
TCTGTATATA ACATTGTCCT CATCAGCTAT GATCGATACC TGTCACTCTC AAATGCTGTG 360  
TCTTATAGAA CTCAACATAC TGGGGCTTG AAGATTGTTA CTCTGATGGT GGCGTTGG 420  
GTGCTGGCCT TCTTAGTGAA TGGGCCAATG ATTCTAGTTT CAGAGTCTTG GAAGGATGAA 480  
GGTAGTGAAT GTGAACCTGG ATTTTTTCG GAATGGTACA TCCTTGCCAT CACATCATTG 540  
20 TTGGAATTAG TGATCCCAGT CATCTTAGTC GCTTATTCA ACATGAATAT TTATTGGAGC 600  
CTGTGGAAGC GTGATCATCT CAGTAGGTGC CAAAGCCATC CTGGACTGAC TGCTGCTCT 660  
TCCAACATCT GTGGACACTC ATTCAAGAGT AGACTATCTT CAAGGAGATC TCTTCTGCA 720  
TCGACAGAAG TTCCTGCATC CTTTCATTCA GAGAGACAGA GGAGAAAGAG TAGTCTCATG 780  
TTTCCTCAA GAACCAAGAT GAATAGCAAT ACAATTGCTT CCAAAATGGG TTCCTCTCC 840  
25 CAATCAGATT CTGTAGCTCT TCACCAAAGG GAACATGTTG AACTGCTTAG AGCCAGGAGA 900  
TTAGCCAAGT CACTGGCCAT TCTCTTAGGG GTTTTGCTG TTTGCTGGC TCCATATTCT 960  
CTGTTCACAA TTGTCCTTTC ATTTTATTCC TCAGCAACAG GTCCTAAATC AGTTGGTAT 1020  
AGAATTGCAT TTTGGCTTCA GTGGTTCAAT TCCTTGTCA ATCCTTTTT GTATCCATTG 1080  
TGTCACAAGC GCTTCAAAA GGCTTCTTG AAAATTTT GTATAAAAAA GCAACCTCTA 1140  
30 CCATCACAAAC ACAGTCGGTC AGTATCTTCT TAA 1173

## (15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 390 amino acids  
(B) TYPE: amino acid  
5 (C) STRANDEDNESS:  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Pro Asp Thr Asn Ser Thr Ile Asn Leu Ser Leu Ser Thr Arg Val  
10 1 5 10 15

Thr Leu Ala Phe Phe Met Ser Leu Val Ala Phe Ala Ile Met Leu Gly  
20 25 30

Asn Ala Leu Val Ile Leu Ala Phe Val Val Asp Lys Asn Leu Arg His  
35 40 45

15 Arg Ser Ser Tyr Phe Phe Leu Asn Leu Ala Ile Ser Asp Phe Phe Val  
50 55 60

Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe Glu Trp  
65 70 75 80

Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp Tyr Leu  
20 85 90 95

Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr Asp Arg  
100 105 110

Tyr Leu Ser Val Ser Asn Ala Val Ser Tyr Arg Thr Gln His Thr Gly  
115 120 125

25 Val Leu Lys Ile Val Thr Leu Met Val Ala Val Trp Val Leu Ala Phe  
130 135 140

Leu Val Asn Gly Pro Met Ile Leu Val Ser Glu Ser Trp Lys Asp Glu  
145 150 155 160

Gly Ser Glu Cys Glu Pro Gly Phe Phe Ser Glu Trp Tyr Ile Leu Ala  
30 165 170 175

Ile Thr Ser Phe Leu Glu Phe Val Ile Pro Val Ile Leu Val Ala Tyr  
180 185 190

Phe Asn Met Asn Ile Tyr Trp Ser Leu Trp Lys Arg Asp His Leu Ser  
195 200 205

35 Arg Cys Gln Ser His Pro Gly Leu Thr Ala Val Ser Ser Asn Ile Cys  
210 215 220

Gly His Ser Phe Arg Gly Arg Leu Ser Ser Arg Arg Ser Leu Ser Ala  
225 230 235 240

Ser Thr Glu Val Pro Ala Ser Phe His Ser Glu Arg Gln Arg Arg Lys  
245 250 255

5 Ser Ser Leu Met Phe Ser Ser Arg Thr Lys Met Asn Ser Asn Thr Ile  
260 265 270

Ala Ser Lys Met Gly Ser Phe Ser Gln Ser Asp Ser Val Ala Leu His  
275 280 285

Gln Arg Glu His Val Glu Leu Leu Arg Ala Arg Arg Leu Ala Lys Ser  
10 290 295 300

Leu Ala Ile Leu Leu Gly Val Phe Ala Val Cys Trp Ala Pro Tyr Ser  
305 310 315 320

Leu Phe Thr Ile Val Leu Ser Phe Tyr Ser Ser Ala Thr Gly Pro Lys  
325 330 335

15 Ser Val Trp Tyr Arg Ile Ala Phe Trp Leu Gln Trp Phe Asn Ser Phe  
340 345 350

Val Asn Pro Leu Leu Tyr Pro Leu Cys His Lys Arg Phe Gln Lys Ala  
355 360 365

Phe Leu Lys Ile Phe Cys Ile Lys Lys Gln Pro Leu Pro Ser Gln His  
20 370 375 380

Ser Arg Ser Val Ser Ser  
385 390

## (16) INFORMATION FOR SEQ ID NO:15:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1128 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGGCGAACG CGAGCGAGCC GGGTGGCAGC GGCGGGCG AGGCAGGCC CCTGGGCCTC 60  
AAGCTGGCCA CGCTCAGCCT GCTGCTGTGC GTGAGCCTAG CGGGCAACGT GCTGTTGCG 120  
CTGCTGATCG TGCGGGAGCG CAGCCTGCAC CGCGCCCCGT ACTACCTGCT GCTCGACCTG 180  
TGCCTGGCCG ACGGGCTGCG CGCGCTCGCC TGCCTCCGG CCGTCATGCT GGCGCGCGG 240  
35 CGTGCGGCCGG CCGCGGCCGG GGCGCCGCCG GGCGCGCTGG GCTGCAAGCT GCTCGCCTTC 300

CTGGCCGCGC TCTTCTGCTT CCACGCCGCC TTCCTGCTGC TGGCGTGGG CGTCACCCGC 360  
TACCTGGCCA TCGCGCACCA CCGCTTCTAT GCAGAGCGCC TGGCCGGCTG GCCGTGCGCC 420  
GCCATGCTGG TGTGCGCCGC CTGGCGCTG GCGCTGGCCG CGGCCTTCCC GCCAGTGCTG 480  
GACGGCGGTG GCGACGACGA GGACGCGCCG TGCGCCCTGG AGCAGCGGCC CGACGGCGCC 540  
5 CCCGGCGCGC TGGGCTTCCT GCTGCTGCTG GCCGTGGTGG TGGGCGCCAC GCACCTCGTC 600  
TACCTCCGCC TGCTCTTCTT CATCCACGAC CGCCGCAAGA TGCGGCCCCGC GCGCCTGGTG 660  
CCCGCCGTCA GCCACGACTG GACCTTCCAC GGCCCAGGGCG CCACCGGCCA GGCGGCCGCC 720  
AACTGGACGG CGGGCTTCGG CCGCGGGCCC ACGCCGCCCG CGCTTGTGGG CATCGGGCCC 780  
GCAGGGCCGG GCCGCGGCCGC GCGCCGCCTC CTCGTGCTGG AAGAATTCAA GACGGAGAAG 840  
10 AGGCTGTGCA AGATGTTCTA CGCCGTCACG CTGCTCTTCC TGCTCCTCTG GGGGCCCTAC 900  
GTCGTGGCCA GCTACCTGCG GGTCTGGTG CGGCCCGGCG CCGTCCCCCA GGCCTACCTG 960  
ACGGCCTCCG TGTGGCTGAC CTTCGCGCAG GCCGGCATCA ACCCCGTCGT GTGCTTCCTC 1020  
TTCAACAGGG AGCTGAGGGA CTGCTTCAGG GCCCAGTTCC CCTGCTGCCA GAGCCCCCGG 1080  
ACCACCCAGG CGACCCATCC CTGCGACCTG AAAGGCATTG GTTTATGA 1128

## 15 (17) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 375 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
20 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala Asn Ala Ser Glu Pro Gly Gly Ser Gly Gly Gly Glu Ala Ala  
1 5 10 15

25 Ala Leu Gly Leu Lys Leu Ala Thr Leu Ser Leu Leu Leu Cys Val Ser  
20 25 30

Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser  
35 40 45

30 Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp  
50 55 60

Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg  
65 70 75 80

Arg Ala Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys  
85 90 95

Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu  
100 105 110

5 Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg  
115 120 125

Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val  
130 135 140

10 Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Ala Phe Pro Pro Val Leu  
145 150 155 160

Asp Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg  
165 170 175

Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Ala Val  
180 185 190

15 Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile  
195 200 205

His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser  
210 215 220

20 His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala Ala Ala  
225 230 235 240

Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val  
245 250 255

Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val  
260 265 270

25 Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala  
275 280 285

Val Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val Ala Ser  
290 295 300

Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu  
305 310 315 320

30 Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn Pro Val  
325 330 335

Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln  
340 345 350

35 Phe Pro Cys Cys Gln Ser Pro Arg Thr Thr Gln Ala Thr His Pro Cys  
355 360 365

Asp Leu Lys Gly Ile Gly Leu

370

375

## (18) INFORMATION FOR SEQ ID NO:17:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1002 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

10 ATGAACACCA CAGTGATGCA AGGCTTCAAC AGATCTGAGC GGTGCCCGAG AGACACTCGG 60  
ATAGTACAGC TGGTATTCCC AGCCCTCTAC ACAGTGGTTT TCTTGACCGG CATCCTGCTG 120  
AATACTTTGG CTCTGTGGGT GTTTGTTCAC ATCCCCAGCT CCTCCACCTT CATCATCTAC 180  
CTCAAAAACA CTTTGGTGGC CGACTTGATA ATGACACTCA TGCTTCCTTT CAAAATCCTC 240  
TCTGACTCAC ACCTGGCACC CTGGCAGCTC AGAGCTTTG TGTGTCGTTT TTCTTCGGTG 300  
15 ATATTTTATG AGACCATGTA TGTGGGCATC GTGCTGTTAG GGCTCATAGC CTTTGACAGA 360  
TTCCTCAAGA TCATCAGACC TTTGAGAAAT ATTTTTCTAA AAAAACCTGT TTTTGCAAAA 420  
ACGGTCTCAA TCTTCATCTG GTTCTTTTG TTCTTCATCT CCCTGCCAAA TACGATCTG 480  
AGCAACAAGG AAGCAACACC ATCGTCTGTG AAAAAGTGTG CTTCCCTAAA GGGGCCTCTG 540  
GGGCTGAAAT GGCATCAAAT GGTAAATAAC ATATGCCAGT TTATTTCTG GACTGTTTTT 600  
20 ATCCTAATGC TTGTGTTTA TGTGGTTATT GCAAAAAAAG TATATGATTG TTATAGAAAG 660  
TCCAAAAGTA AGGACAGAAA AAACAACAAA AAGCTGGAAG GCAAAGTATT TGTTGTCGTG 720  
GCTGTCTTCT TTGTGTTTT TGCTCCATTG CATTGAGCA GAGTTCCATA TACTCACAGT 780  
CAAACCAACA ATAAGACTGA CTGTAGACTG CAAAATCAAC TGTTTATTGC TAAAGAAACA 840  
ACTCTCTTTT TGGCAGCAAC TAACATTTGT ATGGATCCCT TAATATACAT ATTCTTATGT 900  
25 AAAAATTCA CAGAAAAGCT ACCATGTATG CAAGGGAGAA AGACCACAGC ATCAAGCCAA 960  
GAAAATCATA GCAGTCAGAC AGACAACATA ACCTTAGGCT GA 1002

## (19) INFORMATION FOR SEQ ID NO:18:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 333 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

	Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro			
5	1	5	10	15
	Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val			
	20	25	30	
	Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe			
	35	40	45	
10	Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr			
	50	55	60	
	Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu			
	65	70	75	80
15	Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg			
	85	90	95	
	Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu			
	100	105	110	
	Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu			
	115	120	125	
20	Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile			
	130	135	140	
	Phe Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu			
	145	150	155	160
25	Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu			
	165	170	175	
	Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys			
	180	185	190	
	Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val			
	195	200	205	
30	Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys			
	210	215	220	
	Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val			
	225	230	235	240
35	Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro			
	245	250	255	

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn  
260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn  
275 280 285

5 Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr  
290 295 300

Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln  
305 310 315 320

Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly  
10 325 330

## (20) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1122 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGGCCAACA CTACCGGAGA GCCTGAGGAG GTGAGCGGCG CTCTGTCCCC ACCGTCCGCA 60  
20 TCAGCTTATG TGAAGCTGGT ACTGCTGGG A CTGATTATGT GCGTGAGCCT GGCGGGTAAC 120  
GCCATCTTGT CCCTGCTGGT GCTCAAGGAG CGTGCCCTGC ACAAGGCTCC TTACTACTTC 180  
CTGCTGGACC TGTGCCTGGC CGATGGCATA CGCTCTGCCG TCTGCTTCCC CTTTGTGCTG 240  
GCTTCTGTGC GCCACGGCTC TTCATGGACC TTCAGTGCAC TCAGCTGCAA GATTGTGGCC 300  
TTTATGGCCG TGCTCTTTG CTTCCATGCG GCCTTCATGC TGTTCTGCAT CAGCGTCACC 360  
25 CGCTACATGG CCATCGCCCA CCACCGCTTC TACGCCAAGC GCATGACACT CTGGACATGC 420  
GCGGCTGTCA TCTGCATGGC CTGGACCCTG TCTGTGGCCA TGGCCTTCCC ACCTGTCTTT 480  
GACGTGGGCA CCTACAAGTT TATTGGGAG GAGGACCAAGT GCATCTTGA GCATCGCTAC 540  
TTCAAGGCCA ATGACACGCT GGGCTTCATG CTTATGTTGG CTGTGCTCAT GGCAGCTACC 600  
CATGCTGTCT ACGGCAAGCT GCTCCTCTTC GAGTATCGTC ACCGCAAGAT GAAGCCAGTG 660  
30 CAGATGGTGC CAGCCATCAG CCAGAACTGG ACATTCCATG GTCCCAGGGC CACCGGCCAG 720  
GCTGCTGCCA ACTGGATCGC CGGCTTGGC CGTGGGCCA TGCCACCAAC CCTGCTGGGT 780  
ATCCGGCAGA ATGGGCATGC AGCCAGCCGG CGGCTACTGG GCATGGACGA GGTCAAGGGT 840

GAAAAGCAGC TGGGCCGCAT GTTCTACGCG ATCACACTGC TCTTTCTGCT CCTCTGGTCA 900  
CCCTACATCG TGGCCTGCTA CTGGCGAGTG TTTGTGAAAG CCTGTGCTGT GCCCCACCGC 960  
TACCTGGCCA CTGCTGTTG GATGAGCTTC GCCCAGGCTG CCGTCAACCC AATTGTCTGC1020  
TTCCTGCTCA ACAAGGACCT CAAGAAGTGC CTGACCACTC ACGCCCCCTG CTGGGGCACA1080  
5 GGAGGTGCC CGGCTCCCAG AGAACCTAC TGTGTCATGT GA 1122

## (21) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 373 amino acids  
(B) TYPE: amino acid  
10 (C) STRANDEDNESS:  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser  
15 1 5 10 15  
Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile  
20 20 25 30  
Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu  
25 35 40 45  
Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu  
30 50 55 60  
Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu  
35 65 70 75 80  
Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys  
40 85 90 95  
Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe  
45 100 105 110  
Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His  
50 115 120 125  
Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile  
55 130 135 140  
Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe  
60 145 150 155 160  
Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe  
65 165 170 175  
35

Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met  
180 185 190

Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu  
195 200 205

5 Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro  
210 215 220

Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln  
225 230 235 240

Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro  
10 245 250 255

Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu  
260 265 270

Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe  
275 280 285

15 Tyr Ala Ile Thr Leu Leu Phe Leu Leu Trp Ser Pro Tyr Ile Val  
290 295 300

Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg  
305 310 315 320

Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn  
20 325 330 335

Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Thr  
340 345 350

Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu  
355 360 365

25 Pro Tyr Cys Val Met  
370

## (22) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1053 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

35 ATGGCTTG AACAGAACCA GTCAACAGAT TATTATTATG AGGAAAATGA AATGAATGGC 60  
ACTTATGACT ACAGTCAATA TGAATTGATC TGTATCAAAG AAGATGTCAG AGAATTTGCA 120

AAAGTTTCC TCCCTGTATT CCTCACAATA GCTTCGTCA TTGGACTTGC AGGCAATTCC 180  
ATGGTAGTGG CAATTTATGC CTATTACAAG AAACAGAGAA CCAAAACAGA TGTGTACATC 240  
CTGAATTGG CTGTAGCAGA TTTACTCCTT CTATTCACTC TGCCCTTTG GGCTGTTAAT 300  
GCAGTTCATG GGTGGGTTT AGGGAAAATA ATGTGAAAAA TAACTTCAGC CTTGTACACA 360  
5 CTAAACTTTG TCTCTGGAAT GCAGTTCTG GCTTGCATCA GCATAGACAG ATATGTGGCA 420  
GTAACATAATG TCCCCAGCCA ATCAGGAGTG GGAAAACCAT GCTGGATCAT CTGTTCTGT 480  
GTCTGGATGG CTGCCATCTT GCTGAGCATA CCCAGCTGG TTTTTATAC AGTAAATGAC 540  
AATGCTAGGT GCATTCCCAT TTTCCCCGC TACCTAGGAA CATCAATGAA AGCATTGATT 600  
CAAATGCTAG AGATCTGCAT TGGATTGTA GTACCCTTTC TTATTATGGG GGTGTGCTAC 660  
10 TTTATCACGG CAAGGACACT CATGAAGATG CCAAACATTA AAATATCTG ACCCTAAAAA 720  
GTTCTGCTCA CAGTCGTTAT AGTTTCATT GTCACTCAAC TGCCTTATAA CATTGTCAAG 780  
TTCTGCCAG CCATAGACAT CATCTACTCC CTGATCACCA GCTGCAACAT GAGCAAACGC 840  
ATGGACATCG CCATCCAAGT CACAGAAAGC ATTGCACTCT TTCACAGCTG CCTCAACCCA 900  
ATCCTTTATG TTTTTATGGG AGCATCTTTC AAAAACTACG TTATGAAAGT GGCCAAGAAA 960  
15 TATGGGTCCCT GGAGAAAGACA GAGACAAAGT GTGGAGGAGT TTCCTTTGA TTCTGAGGGT1020  
CCTACAGAGC CAACCAGTAC TTTAGCATT TAA 1053

## (23) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 350 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

25 Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn  
1 5 10 15  
Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile  
20 25 30  
Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu  
30 35 40 45  
Thr Ile Ala Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala

	50	55	60	
	Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile			
65	65	70	75	80
5	Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Phe Thr Leu Pro Phe			
	85	90	95	
	Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys			
	100	105	110	
	Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln			
	115	120	125	
10	Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Asn Val			
	130	135	140	
	Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys			
145	145	150	155	160
15	Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr			
	165	170	175	
	Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu			
	180	185	190	
	Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly			
	195	200	205	
20	Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala			
	210	215	220	
	Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys			
225	225	230	235	240
25	Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr			
	245	250	255	
	Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile			
	260	265	270	
	Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr			
	275	280	285	
30	Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val			
	290	295	300	
	Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys			
305	305	310	315	320
35	Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe			
	325	330	335	
	Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile			
	340	345	350	

## (24) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1116 base pairs  
(B) TYPE: nucleic acid  
5 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGCCAGGAA ACGCCACCCC AGTGACCACC ACTGCCCGT GGGCCTCCCT GGGCCTCTCC 60  
10 GCCAAGACCT GCAACAACGT GTCCCTCGAA GAGAGCAGGA TAGTCCTGGT CGTGGTGTAC 120  
AGCGCGGTGT GCACGCTGGG GGTGCCGGCC AACTGCCTGA CTGCGTGGCT GGCGCTGCTG 180  
CAGGTACTGC AGGGCAACGT GCTGGCCGTC TACCTGCTCT GCCTGGCACT CTGCGAACTG 240  
CTGTACACAG GCACGCTGCC ACTCTGGGTC ATCTATATCC GCAACCAGCA CCGCTGGACC 300  
CTAGGCCTGC TGGCCTCGAA GGTGACCGCC TACATCTTCT TCTGCAACAT CTACGTCAGC 360  
15 ATCCTCTTCC TGTGCTGCAT CTCCCTGCGAC CGCTTCGTGG CCGTGGTGT A CGCGCTGGAG 420  
AGTCGGGGCC GCCGCCGCCG GAGGACCGCC ATCCTCATCT CCGCCTGCAT CTTCATCCTC 480  
GTCGGGATCG TTCACTACCC GGTGTTCCAG ACGGAAGACA AGGAGACCTG CTTTGACATG 540  
CTGCAGATGG ACAGCAGGAT TGCCGGGTAC TACTACGCCA GGTTCACCGT TGGCTTGCC 600  
ATCCCTCTCT CCATCATCGC CTTCACCAAC CACCGGATTT TCAGGAGCAT CAAGCAGAGC 660  
20 ATGGGCTTAA GCGCTGCCCA GAAGGCCAAG GTGAAGCACT CGGCCATCGC GGTGGTTGTC 720  
ATCTTCCTAG TCTGCTTCGC CCCGTACAC CTGGTTCTCC TCGTCAAAGC CGCTGCCCTT 780  
TCCTACTACA GAGGAGACAG GAACGCCATG TGCGGCTTGG AGGAAAGGCT GTACACAGCC 840  
TCTGTGGTGT TTCTGTGCCT GTCCACGGTG AACGGCGTGG CTGACCCAT TATCTACGTG 900  
CTGGCCACGG ACCATTCCCG CCAAGAAGTG TCCAGAATCC ATAAGGGGTG GAAAGAGTGG 960  
25 TCCATGAAGA CAGACGTCAC CAGGCTCACC CACAGCAGGG ACACCGAGGA GCTGCAGTCG 1020  
CCCGTGGCCC TTGCAGACCA CTACACCTTC TCCAGGCCCG TGCACCCACC AGGGTCACCA 1080  
TGCCCTGCAA AGAGGCTGAT TGAGGAGTCC TGCTGA 1116

## (25) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 371 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Pro Gly Asn Ala Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser  
1 5 10 15

Leu Gly Leu Ser Ala Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser  
20 25 30

10 Arg Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val  
35 40 45

Pro Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln  
50 55 60

Gly Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu  
15 65 70 75 80

Leu Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln  
85 90 95

His Arg Trp Thr Leu Gly Leu Leu Ala Ser Lys Val Thr Ala Tyr Ile  
100 105 110

20 Phe Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser  
115 120 125

Cys Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg  
130 135 140

Arg Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu  
25 145 150 155 160

Val Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr  
165 170 175

Cys Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr  
180 185 190

30 Ala Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe  
195 200 205

Thr Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser  
210 215 220

Ala Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val  
35 225 230 235 240

Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys  
245 250 255

Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly  
260 265 270

5 Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser  
275 280 285

Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp  
290 295 300

His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp  
10 305 310 315 320

Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu  
325 330 335

Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg  
340 345 350

15 Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu  
355 360 365

Glu Ser Cys  
370

## (26) INFORMATION FOR SEQ ID NO:25:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGGCGAACT ATAGCCATGC AGCTGACAAC ATTTGCAAA ATCTCTGCC TCTAACAGCC 60  
TTTCTGAAAC TGACTTCCTT GGGTTTCATA ATAGGAGTCA GCGTGGTGGG CAACCTCCTG 120  
ATCTCCATTG TGCTAGTGAA AGATAAGACC TTGCATAGAG CACCTTACTA CTTCCCTGTTG 180  
30 GATCTTGCT GTTCAGATAT CCTCAGATCT GCAATTGTT TCCCATTTGT GTTCAACTCT 240  
GTCAAAAATG GCTCTACCTG GACTTATGGG ACTCTGACTT GCAAAGTGAT TGCCTTCTG 300  
GGGGTTTGT CCTGTTCCA CACTGCTTTC ATGCTCTTCT GCATCAGTGT CACCAGATAC 360  
TTAGCTATCG CCCATCACCG CTTCTATACA AAGAGGCTGA CCTTTTGGAC GTGTCTGGCT 420  
GTGATCTGTA TGGTGTGGAC TCTGTCTGTG GCCATGGCAT TTCCCCGGT TTTAGACGTG 480

GGCACTTACT CATTCTTGTAG GGAGGAAGAT CAATGCACCT TCCAACACCG CTCCCTTCAGG 540  
GCTAATGATT CCTTAGGATT TATGCTGCTT CTTGCTCTCA TCCTCCTAGC CACACAGCTT 600  
GTCTACCTCA AGCTGATATT TTTCGTCCAC GATCGAAGAA AAATGAAGCC AGTCCAGTTT 660  
GTAGCAGCAG TCAGCCAGAA CTGGACTTTT CATGGTCCTG GAGCCAGTGG CCAGGCAGCT 720  
5 GCCAATTGGC TAGCAGGATT TGGAAGGGT CCCACACCAC CCACCTTGCT GGGCATCAGG 780  
CAAAAATGCAA ACACCACAGG CAGAAGAAGG CTATTGGTCT TAGACGAGTT CAAAATGGAG 840  
AAAAGAACATCA GCAGAATGTT CTATATAATG ACTTTTCTGT TTCTAACCTT GTGGGGCCCC 900  
TACCTGGTGG CCTGTTATTG GAGAGTTTT GCAAGAGGGC CTGTAGTACC AGGGGGATTT 960  
CTAACAGCTG CTGTCTGGAT GAGTTTGCC CAAGCAGGAA TCAATCCTTT TGTCTGCATT1020  
10 TTCTCAAACA GGGAGCTGAG GCGCTGTTTC AGCACAAACCC TTCTTTACTG CAGAAAATCC1080  
AGGTTACCAA GGGAACCTTA CTGTGTTATA TGA 1113

## (27) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
15 (A) LENGTH: 370 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

20 Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser  
1 5 10 15

Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly  
20 25 30

Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp  
25 35 40 45

Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys  
50 55 60

Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser  
65 70 75 80

30 Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val  
85 90 95

Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu

	100	105	110
	Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe		
	115	120	125
5	Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met		
	130	135	140
	Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val		
	145	150	155
	Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His		
	165	170	175
10	Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala		
	180	185	190
	Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe		
	195	200	205
15	Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val		
	210	215	220
	Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala		
	225	230	235
	Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu		
	245	250	255
20	Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu		
	260	265	270
	Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr		
	275	280	285
25	Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala		
	290	295	300
	Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe		
	305	310	315
	Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro		
	325	330	335
30	Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr		
	340	345	350
	Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys		
	355	360	365
35	Val Ile		
	370		

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1080 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCAGGTCC CGAACAGCAC CGGCCGGAC AACGCGACGC TGCAGATGCT GCGGAACCCG 60  
GCGATCGCGG TGGCCCTGCC CGTGGTGTAC TCGCTGGTGG CGGC GGTCAG CATCCC GGCG 120  
10 AACCTCTTCT CTCTGTGGGT GCTGTGCCGG CGCATGGGGC CCAGATCCCC GTCGGT C ATC 180  
TTCATGATCA ACCTGAGCGT CACGGACCTG ATGCTGGCCA GCGTGTGTTGCC TTTCAAATC 240  
TACTACCATT GCAACCGCCA CCACTGGGTA TTCGGGGTGC TGCTTGCAA CGTGGTGACC 300  
GTGGCCTTTT ACGCAAACAT GTATTCCAGC ATCCTCACCA TGACCTGTAT CAGCGTGGAG 360  
CGCTTCCTGG GGGTCCTGTA CCCGCTCAGC TCCAAGCGCT GGCGCCGCCG TCGTTACGCG 420  
15 GTGGCCCGCGT GTGCAGGGAC CTGGCTGCTG CTCCCTGACCG CCCTGTGCCG GCTGGCGCGC 480  
ACCGATCTCA CCTACCCGGT GCACGCCCTG GGCATCATCA CCTGCTTCGA CGTCCTCAAG 540  
TGGACGATGC TCCCCAGCGT GCCATGTGG GCCGTGTTCC TCTTCACCAT CTTCATCCTG 600  
CTGTTCCCTCA TCCCGTTCGT GATCACCGTG GCTTGT TACA CGGCCACCAT CCTCAAGCTG 660  
TTGCGCACGG AGGAGGGCGCA CGGCCGGGAG CAGCGGAGGC GGCGGGTGGG CCTGGCCGCG 720  
20 GTGGTCTTGC TGGCCTTGT CACCTGCTTC GCCCCAAACA ACTTCGTGCT CCTGGCGCAC 780  
ATCGTGAGCC GCCTGTTCTA CGGCAAGAGC TACTACCACG TGTACAAGCT CACGCTGTGT 840  
CTCAGCTGCC TCAACAAC TG TCTGGACCCG TTTGTTATT ACTTTGCCTGC CGGGAAATTC 900  
CAGCTGCC TGCGGGATA TTTGGGCTGC CGCCGGGTGC CCAGAGACAC CCTGGACACG 960  
CGCCGCGAGA GCCTCTTCTC CGCCAGGACC ACGTCCGTGC GCTCCGAGGC CGGTGCGCAC 1020  
25 CCTGAAGGGA TGGAGGGAGC CACCAGGCC GGCCCTCCAGA GGCAGGAGAG TGTGTTCTGA 1080

(29) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 359 amino acids  
(B) TYPE: amino acid  
30 (C) STRANDEDNESS:  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Gln Val Pro Asn Ser Thr Gly Pro Asp Asn Ala Thr Leu Gln Met  
1 5 10 15

5 Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu  
20 25 30

Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu  
35 40 45

Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn  
10 50 55 60

Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile  
65 70 75 80

Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys  
85 90 95

15 Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu  
100 105 110

Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro  
115 120 125

20 Leu Ser Ser Lys Arg Trp Arg Arg Arg Tyr Ala Val Ala Ala Cys  
130 135 140

Ala Gly Thr Trp Leu Leu Leu Thr Ala Leu Cys Pro Leu Ala Arg  
145 150 155 160

Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe  
165 170 175

25 Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val  
180 185 190

Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile  
195 200 205

30 Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu  
210 215 220

Glu Ala His Gly Arg Glu Gln Arg Arg Ala Val Gly Leu Ala Ala  
225 230 235 240

Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val  
245 250 255

35 Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr  
260 265 270

His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu  
275 280 285

Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu  
290 295 300

5 Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr  
305 310 315 320

Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu  
325 330 335

Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu  
10 340 345 350

Gln Arg Gln Glu Ser Val Phe  
355

## (30) INFORMATION FOR SEQ ID NO:29:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1503 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGGAGCGTC CCTGGGAGGA CAGCCCAGGC CCGGAGGGGG CAGCTGAGGG CTCGCCTGTG 60  
CCAGTCGCCG CCGGGGGCGCG CTCCGGTGCC GCGGCGACTG GCACAGGCTG GCAGCCATGG 120  
GCTGAGTGCC CGGGACCCAA GGGGAGGGGG CAACTGCTGG CGACCGCCGG CCCTTGCCT 180  
CGCTGGCCCG CCCCCCTCGCC TGCCAGCTCC AGCCCCGCCC CGGGAGCGGC GTCCGCTCAC 240  
25 TCGGTTCAAG GCAGCGCGAC TGGGGTGGC GCACGACCAG GGCGCAGACC TTGGGGCGCG 300  
CGGCCCATGG AGTCGGGGCT GCTGCGGCCG GCGCCGGTGA GCGAGGTCAT CGTCCTGCAT 360  
TACAACCTACA CCGGCAAGCT CCGCGGTGCG AGCTACCAGC CGGGTGCCGG CCTGCGCGCC 420  
GACGCCGTGG TGTGCCTGGC GGTGTGCGCC TTCATCGTGC TAGAGAACCT AGCCGTGTTG 480  
TTGGTGCTCG GACGCCACCC GCGCTTCCAC GCTCCCATGT TCCTGCTCCT GGGCAGCCTC 540  
30 ACGTTGTCGG ATCTGCTGGC AGGCGCCGCC TACGCCGCCA ACATCCTACT GTCGGGGCCG 600  
CTCACGCTGA AACTGTCCCC CGCGCTCTGG TTTCGCACGGG AGGGAGGCGT CTTCGTGGCA 660  
CTCACTGCGT CCGTGCTGAG CCTCCTGGCC ATCGCGCTGG AGCGCAGCCT CACCATGGCG 720

CGCAGGGGGC CCGCGCCCGT CTCCAGTCGG GGGCGCACGC TGGCGATGGC AGCCGCGGCC 780  
 TGGGGCGTGT CGCTGCTCCT CGGGCTCCTG CCAGCGCTGG GCTGGAATTG CCTGGGTCGC 840  
 CTGGACGCTT GCTCCACTGT CTTGCCGCTC TACGCCAAGG CCTACGTGCT CTTCTGCCGTG 900  
 CTCGCCTTCG TGGGCATCCT GGCCGCGATC TGTGCACTCT ACGCGCGCAT CTACTGCCAG 960  
 5 GTACGCGCCA ACGCGCGCG CCTGCCGGCA CGGCCCGGGA CTGCGGGGAC CACCTCGACC1020  
 CGGGCGCGTC GCAAGCCCG CGCTCTGGCC TTGCTGCGCA CGCTCAGCGT GGTGCTCCTG1080  
 GCCTTTGTGG CATGTTGGGG CCCCCCTCTTC CTGCTGCTGT TGCTCGACGT GGCGTGCCCG1140  
 GCGCGCACCT GTCCTGTACT CCTGCAGGCC GATCCCTTCC TGGGACTGGC CATGGCCAAC1200  
 TCACTTCTGA ACCCCATCAT CTACACGCTC ACCAACCGCG ACCTGCGCCA CGCGCTCCTG1260  
 10 CGCCTGGTCT GCTGCGGACG CCACTCCTGC GGCAGAGACC CGAGTGGCTC CCAGCAGTCG1320  
 GCGAGCGCGG CTGAGGCTTC CGGGGGCCTG CGCCGCTGCC TGCCCCCGGG CCTTGATGGG1380  
 AGCTTCAGCG GCTCGGAGCG CTCATGCC CAGCGCGACG GGCTGGACAC CAGGGCTCC1440  
 ACAGGCAGCC CCGGTGCACC CACAGCCGCC CGGACTCTGG TATCAGAACC GGCTGCAGAC1500  
 TGA 1503

## 15 (31) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- 20 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

	Met	Glu	Arg	Pro	Trp	Glu	Asp	Ser	Pro	Gly	Pro	Glu	Gly	Ala	Ala	Glu
1															15	
25	Gly	Ser	Pro	Val	Pro	Val	Ala	Ala	Gly	Ala	Arg	Ser	Gly	Ala	Ala	Ala
															30	
	Ser	Gly	Thr	Gly	Trp	Gln	Pro	Trp	Ala	Glu	Cys	Pro	Gly	Pro	Lys	Gly
															45	
30	Arg	Gly	Gln	Leu	Leu	Ala	Thr	Ala	Gly	Pro	Leu	Arg	Arg	Trp	Pro	Ala
	Pro	Ser	Pro	Ala	Ser	Ser	Ser	Pro	Ala	Pro	Gly	Ala	Ala	Ser	Ala	His
															80	
65																
70																
75																

09875076 098604

Ser Val Gln Gly Ser Ala Thr Ala Gly Gly Ala Arg Pro Gly Arg Arg  
                   85                     90                     95  
  
 Pro Trp Gly Ala Arg Pro Met Glu Ser Gly Leu Leu Arg Pro Ala Pro  
                   100                    105                    110  
  
 5     Val Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg  
       115                             120                     125  
  
 Gly Ala Ser Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp Ala Val Val  
       130                            135                     140  
  
 10    Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu Ala Val Leu  
       145                            150                     155                    160  
  
 Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met Phe Leu Leu  
       165                            170                     175  
  
 Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala  
       180                            185                     190  
  
 15    Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala  
       195                            200                     205  
  
 Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu Thr Ala Ser  
       210                            215                     220  
  
 20    Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu Thr Met Ala  
       225                            230                     235                    240  
  
 Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr Leu Ala Met  
       245                            250                     255  
  
 Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Gly Leu Leu Pro Ala  
       260                            265                     270  
  
 25    Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser Thr Val Leu  
       275                            280                     285  
  
 Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu Ala Phe Val  
       290                            295                     300  
  
 30    Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln  
       305                            310                     315                    320  
  
 Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly  
       325                            330                     335  
  
 Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu  
       340                            345                     350  
  
 35    Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro  
       355                            360                     365  
  
 Leu Phe Leu Leu Leu Leu Asp Val Ala Cys Pro Ala Arg Thr Cys

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	370	375	380
	Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn		
	385	390	395
	Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg		
5	405	410	415
	His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg		
	420	425	430
	Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly		
	435	440	445
10	Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly		
	450	455	460
	Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser		
	465	470	475
	Thr Gly Ser Pro Gly Ala Pro Thr Ala Ala Arg Thr Leu Val Ser Glu		
15	485	490	495
	Pro Ala Ala Asp		
	500		

## (32) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- |    |                             |
|----|-----------------------------|
| 20 | (A) LENGTH: 1029 base pairs |
|    | (B) TYPE: nucleic acid      |
|    | (C) STRANDEDNESS: single    |
|    | (D) TOPOLOGY: linear        |

(ii) MOLECULE TYPE: DNA (genomic)

## (25) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGCAAGCCG TCGACAATCT CACCTCTGCG CCTGGAAACA CCAGTCTGTG CACCAGAGAC 60  
TACAAAATCA CCCAGGTCT CTTCCCCACTG CTCTACACTG TCCTGTTTTT TGTTGGACTT 120  
ATCACAAATG GCCTGGCGAT GAGGATTTTC TTTCAAATCC GGAGTAAATC AAACTTTATT 180  
ATTTTTCTTA AGAACACAGT CATTCTGAT CTTCTCATGA TTCTGACTTT TCCATTCAAA 240  
30 ATTCTTAGTG ATGCCAAACT GGGAACAGGA CCACTGAGAA CTGGTGTG TCAAGTTACC 300  
TCCGTATAT TTTATTCAC AATGTATATC AGTATTTCAT TCCTGGACT GATAACTATC 360  
GATCGCTACC AGAAGACCAC CAGGCCATT AAAACATCCA ACCCCAAAAA TCTCTGGGG 420  
GCTAAGATTC TCTCTGTTGT CATCTGGCA TTCATGTTCT TACTCTCTT GCCTAACATG 480

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ATTCTGACCA ACAGGCAGCC GAGAGACAAG AATGTGAAGA AATGCTCTT CCTTAAATCA 540  
GAGTTCGGTC TAGTCTGGCA TGAAATAGTA AATTACATCT GTCAAGTCAT TTTCTGGATT 600  
AATTCTTAA TTGTTATTGT ATGTTATACA CTCATTACAA AAGAACTGTA CCGGTACATAC 660  
GTAAGAACGA GGGGTGAGG TAAAGTCCCC AGGAAAAGG TGAACGTCAA AGTTTCATT 720  
5 ATCATTGCTG TATTCTTAT TTGTTTGTT CCTTCCATT TTGCCGAAT TCCTTACACC 780  
CTGAGCCAAA CCCGGATGT CTTTGACTGC ACTGCTGAAA ATACTCTGTT CTATGTGAAA 840  
GAGAGCACTC TGTGGTTAAC TTCCTTAAAT GCATGCCGG ATCCGTTCAT CTATTTTTC 900  
CTTTGCAAGT CCTTCAGAAA TTCCTTGATA AGTATGCTGA AGTGCCTCAA TTCTGCAACA 960  
TCTCTGTCCC AGGACAATAG GAAAAAAGAA CAGGATGGTG GTGACCCAAA TGAAGAGACT1020

10 CCAATGTAA

1029

## (33) INFORMATION FOR SEQ ID NO:32:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 342 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu  
20 1 5 10 15

Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr  
20 25 30

Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg  
35 40 45

25 Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys  
50 55 60

Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys  
65 70 75 80

30 Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val  
85 90 95

Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile  
100 105 110

Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg

	115	120	125
	Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu		
	130	135	140
	Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met		
5	145	150	155
	Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser		
	165	170	175
	Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr		
	180	185	190
10	Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys		
	195	200	205
	Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg		
	210	215	220
15	Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile		
	225	230	235
	Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg		
	245	250	255
	Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala		
	260	265	270
20	Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser		
	275	280	285
	Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser		
	290	295	300
	Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr		
25	305	310	315
	Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro		
	325	330	335
	Asn Glu Glu Thr Pro Met		
	340		

## 30 (34) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1077 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTCGGTCT GCTACCGTCC CCCAGGGAAC GAGACACTGC TGAGCTGGAA GACTTCGGG 60  
 GCCACAGGCA CAGCCTTCCT GCTGCTGGCG GCGCTGCTGG GGCTGCCTGG CAACGGCTTC 120  
 GTGGTGTGGA GCTTGGCGGG CTGGCGGCCT GCACGGGGC GACCGCTGGC GGCCACGCTT 180  
 5 GTGCTGCACC TGGCGCTGGC CGACGGCGCG GTGCTGCTGC TCACGCCGCT CTTTGTGGCC 240  
 TTCCTGACCC GGCAGGCCTG GCGCGCTGGC CAGGCGGGCT GCAAGGGCGGT GTACTACGTG 300  
 TGCGCGCTCA GCATGTACGC CAGCGTGCTG CTCACCGGCC TGCTCAGCCT GCAGCGCTGC 360  
 CTCGCAGTCA CCCGCCCCCTT CCTGGCGCCT CGGCTGCGCA GCCCGGGCCCT GGCCCGCCGC 420  
 CTGCTGCTGG CGGTCTGGCT GGCCGCCCTG TTGCTCGCCG TCCCAGGCCGC CGTCTACCGC 480  
 10 CACCTGTGGA GGGACCGCGT ATGCCAGCTG TGCCACCCGT CGCCGGTCCA CGCCGCCGCC 540  
 CACCTGAGCC TGGAGACTCT GACCGCTTTC GTGCTTCCTT TCGGGCTGAT GCTCGGCTGC 600  
 TACAGCGTGA CGCTGGCACG GCTGGGGGGC GCGCGCTGGG GCTCCGGGGCG GCACGGGGCG 660  
 CGGGTGGGCC GGCTGGTGAG CGCCATCGTG CTTGCCTTCG GCTTGCTCTG GGCCCCCTAC 720  
 CACGCAGTCA ACCTTCTGCA GGCGGTGCGA GCGCTGGCTC CACCGGAAGG GGCTTGGCG 780  
 15 AAGCTGGCG GAGCCGGCCA GGCGGCGCGA GCGGAACTA CGGCCTTGGC CTTCTTCAGT 840  
 TCTAGCGTCA ACCCGGTGCT CTACGTCTTC ACCGCTGGAG ATCTGCTGCC CGGGCAGGT 900  
 CCCCCTTCC TCACGCGGCT CTTCGAAGGC TCTGGGGAGG CCCGAGGGGG CGGCCGCTCT 960  
 AGGGAAGGGA CCATGGAGCT CGAACTACC CCTCAGCTGA AAGTGGTGGG GCAGGGCCGC 1020  
 GGCAATGGAG ACCCGGGGGG TGGGATGGAG AAGGACGGTC CGGAATGGGA CCTTTGA 1077

## 20 (35)- INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

## 25 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Ser	Val	Cys	Tyr	Arg	Pro	Pro	Gly	Asn	Glu	Thr	Leu	Leu	Ser	Trp
1															15

30 Lys Thr Ser Arg Ala Thr Gly Thr Ala Phe Leu Leu Leu Ala Ala Leu

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	20	25	30
	Leu Gly Leu Pro Gly Asn Gly Phe Val Val Trp Ser Leu Ala Gly Trp		
	35	40	45
5	Arg Pro Ala Arg Gly Arg Pro Leu Ala Ala Thr Leu Val Leu His Leu		
	50	55	60
	Ala Leu Ala Asp Gly Ala Val Leu Leu Thr Pro Leu Phe Val Ala		
	65	70	75
	Phe Leu Thr Arg Gln Ala Trp Pro Leu Gly Gln Ala Gly Cys Lys Ala		
	85	90	95
10	Val Tyr Tyr Val Cys Ala Leu Ser Met Tyr Ala Ser Val Leu Leu Thr		
	100	105	110
	Gly Leu Leu Ser Leu Gln Arg Cys Leu Ala Val Thr Arg Pro Phe Leu		
	115	120	125
15	Ala Pro Arg Leu Arg Ser Pro Ala Leu Ala Arg Arg Leu Leu Ala		
	130	135	140
	Val Trp Leu Ala Ala Leu Leu Ala Val Pro Ala Ala Val Tyr Arg		
	145	150	155
	160		
	His Leu Trp Arg Asp Arg Val Cys Gln Leu Cys His Pro Ser Pro Val		
	165	170	175
20	His Ala Ala Ala His Leu Ser Leu Glu Thr Leu Thr Ala Phe Val Leu		
	180	185	190
	Pro Phe Gly Leu Met Leu Gly Cys Tyr Ser Val Thr Leu Ala Arg Leu		
	195	200	205
25	Arg Gly Ala Arg Trp Gly Ser Gly Arg His Gly Ala Arg Val Gly Arg		
	210	215	220
	Leu Val Ser Ala Ile Val Leu Ala Phe Gly Leu Leu Trp Ala Pro Tyr		
	225	230	235
	240		
	His Ala Val Asn Leu Leu Gln Ala Val Ala Leu Ala Pro Pro Glu		
	245	250	255
30	Gly Ala Leu Ala Lys Leu Gly Gly Ala Gly Gln Ala Ala Arg Ala Gly		
	260	265	270
	Thr Thr Ala Leu Ala Phe Phe Ser Ser Ser Val Asn Pro Val Leu Tyr		
	275	280	285
	Val Phe Thr Ala Gly Asp Leu Leu Pro Arg Ala Gly Pro Arg Phe Leu		
35	290	295	300
	Thr Arg Leu Phe Glu Gly Ser Gly Glu Ala Arg Gly Gly Gly Arg Ser		
	305	310	315
	320		

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Arg Glu Gly Thr Met Glu Leu Arg Thr Thr Pro Gln Leu Lys Val Val  
325 330 335

Gly Gln Gly Arg Gly Asn Gly Asp Pro Gly Gly Met Glu Lys Asp  
340 345 350

5 Gly Pro Glu Trp Asp Leu  
355

(36) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs  
10 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

15 ATGCTGGGGA TCATGGCATG GAATGCAAAT TGCAAAAATC GGCTGGCAGC AGAGGCTGCC 60  
CTGGAAAAGT ACTACCTTTC CATTTTTAT GGGATTGAGT TCGTTGTGGG AGTCCTTGGA 120  
AATACCATTG TTGTTTACGG CTACATCTTC TCTCTGAAGA ACTGGAACAG CAGTAATATT 180  
TATCTCTTAA ACCTCTCTGT CTCTGACTTA GCTTTCTGT GCACCCTCCC CATGCTGATA 240  
AGGAGTTATG CCAATGGAAA CTGGATATAT GGAGACGTGC TCTGCATAAG CAACCGATAT 300  
20 GTGCTTCATG CCAACCTCTA TACCAGCATT CTCTTCTCA CTTTTATCAG CATAGATCGA 360  
TAC TTGATAA TTAAGTATCC TTTCCGAGAA CACCTCTGC AAAAGAAAGA GTTTGCTATT 420  
TTAATCTCCT TGGCCATTTG GGTTTTAGTA ACCTTAGAGT TACTACCCAT ACTTCCCCTT 480  
ATAAAATCCTG TTATAACTGA CAATGGCACC ACCTGTAATG ATTTTGCAAG TTCTGGAGAC 540  
CCCCAACTACA ACCTCATTAA CAGCATGTGT CTAACACTGT TGGGGTTCCCT TATTCCCTTT 600  
25 TTGTTGATGT GTTTCTTTTA TTACAAGATT GCTCTCTTCC TAAAGCAGAG GAATAGGCAG 660  
GTTGCTACTG CTCTGCCCT TGAAAAGCCT CTCAACTTGG TCATCATGGC AGTGGTAATC 720  
TTCTCTGTGC TTGTTACACC CTATCACGTC ATGCGGAATG TGAGGATCGC TTCACCCCTG 780  
GGGAGTTGGA AGCAGTATCA GTGCACTCAG GTCGTATCA ACTCCTTTA CATTGTGACA 840  
CGGCCTTTGG CCTTTCTGAA CAGTGTATC AACCCGTCT TCTATTTCT TTTGGGAGAT 900  
30 CACTTCAGGG ACATGCTGAT GAATGCAAATG AGACACAACT TCAAATCCCT TACATCCTT 960  
AGCAGATGGG CTCATGAACT CCTACTTTCA TTCAGAGAAA AGTGA

1005

0907026-056634

## (37) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 334 amino acids  
(B) TYPE: amino acid  
5 (C) STRANDEDNESS:  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala  
10 1 5 10 15

Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile  
20 20 25 30

Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr  
35 35 40 45

15 Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn  
50 55 60

Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile  
65 65 70 75 80

Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile  
20 85 90 95

Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe  
100 100 105 110

Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe  
115 115 120 125

25 Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu  
130 130 135 140

Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu  
145 145 150 155 160

Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala  
30 165 165 170 175

Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr  
180 180 185 190

Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr  
195 195 200 205

35 Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala  
210 210 215 220

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Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile  
225 230 235 240

Phe Ser Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile  
245 250 255

5 Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val  
260 265 270

Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser  
275 280 285

10 Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp  
290 295 300

Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe  
305 310 315 320

Ser Arg Trp Ala His Glu Leu Leu Ser Phe Arg Glu Lys  
325 330

## 15 (38) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1296 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
20 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
- ATGCAGGCGC TTAACATTAC CCCGGAGCAG TTCTCTCGGC TGCTGCGGGA CCACAAACCTG 60  
ACGCGGGAGC AGTTCATCGC TCTGTACCGG CTGCGACCGC TCGTCTACAC CCCAGAGCTG 120  
25 CCGGGACGCG CCAAGCTGGC CCTCGTGCTC ACCGGCGTGC TCATCTTCGC CCTGGCGCTC 180  
TTTGGCAATG CTCTGGTGTGTT CTACGTGGTG ACCCGCAGCA AGGCCATGCG CACCGTCACC 240  
AACATCTTA TCTGCTCCTT GGCGCTCAGT GACCTGCTCA TCACCTTCTT CTGCATTCCC 300  
GTCACCATGC TCCAGAACAT TTCCGACAAC TGGCTGGGGG GTGCTTTCAT TTGCAAGATG 360  
GTGCCATTTG TCCAGTCTAC CGCTGTTGTG ACAGAAATGC TCACTATGAC CTGCATTGCT 420  
30 GTGGAAAGGC ACCAGGGACT TGTGCATCCT TTTAAAATGA AGTGGCAATA CACCAACCGA 480  
AGGGCTTTCA CAATGCTAGG TGTGGTCTGG CTGGTGGCAG TCATCGTAGG ATCACCCATG 540  
TGGCACGTGC AACAACTTGA GATCAAATAT GACTTCCTAT ATGAAAAGGA ACACATCTGC 600  
TGCTTAGAAG AGTGGACCAAG CCCTGTGCAC CAGAAGATCT ACACCACCTT CATCCTTGTC 660

ATCCTCTTCC TCCTGCCTCT TATGGTGATG CTTATTCTGT ACAGTAAAAT TGGTTATGAA 720  
CTTTGGATAA AGAAAAGAGT TGGGGATGGT TCAGTGCTTC GAACTATTCA TGGAAAAGAA 780  
ATGTCCAAAA TAGCCAGGAA GAAGAACGA GCTGTCATTA TGATGGTGAC AGTGGTGGCT 840  
CTCTTGCTG TGTGCTGGC ACCATTCCAT GTTGTCCATA TGATGATTGA ATACAGTAAT 900  
5 TTTGAAAAGG AATATGATGA TGTCACAATC AAGATGATTT TTGCTATCGT GCAAATTATT 960  
GGATTTCCA ACTCCATCTG TAATCCCATT GTCTATGCAT TTATGAATGA AAACCTCAAA1020  
AAAAATGTTT TGTCTGCAGT TTGTTATTGC ATAGTAAATA AAACCTTCTC TCCAGCACAA1080  
AGGCATGGAA ATTCAAGGAAT TACAATGATG CGGAAGAAAG CAAAGTTTC CCTCAGAGAG1140  
AATCCAGTGG AGGAAACCAA AGGAGAAGCA TTCAGTGATG GCAACATTGA AGTCAAATTG1200  
10 TGTGAACAGA CAGAGGAGAA GAAAAAGCTC AAACGACATC TTGCTCTCTT TAGGTCTGAA1260  
CTGGCTGAGA ATTCTCCTTT AGACAGTGGG CATTAA 1296

## (39) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
15 (A) LENGTH: 431 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

20 Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg  
1 5 10 15

Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg  
20 25 30

25 Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu  
35 40 45

Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala  
50 55 60

Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr  
65 70 75 80

30 Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe  
85 90 95

Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu

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	100	105	110
	Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala		
	115	120	125
5	Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His		
	130	135	140
	Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg		
	145	150	155
	Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val		
	165	170	175
10	Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe		
	180	185	190
	Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro		
	195	200	205
15	Val His Gln Lys Ile Tyr Thr Phe Ile Leu Val Ile Leu Phe Leu		
	210	215	220
	Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu		
	225	230	240
	Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile		
	245	250	255
20	His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Arg Ala Val		
	260	265	270
	Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro		
	275	280	285
25	Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu		
	290	295	300
	Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile		
	305	310	315
	320		
	Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn		
	325	330	335
30	Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val		
	340	345	350
	Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr		
	355	360	365
35	Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu		
	370	375	380
	Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu		
	385	390	395
	400		

Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu  
 405 410 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His  
 420 425 430

5 (40) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

10 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

**CTGTGTACAG CAGTTCGCAG AGTG**

24

(41) INFORMATION FOR SEQ ID NO:40:

- 15       (i) SEQUENCE CHARACTERISTICS:  
            (A) LENGTH: 24 base pairs  
            (B) TYPE: nucleic acid  
            (C) STRANDEDNESS: single  
            (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

**GAGTGCCAGG CAGAGCAGGT AGAC**

24

(42) INFORMATION FOR SEQ ID NO:41:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCGAATTCC TGCTTGCTCC CAGCTTGGCC C

31

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
5 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGTGGATCCT GCTGTCAAAG GTCCCATTCC GG

32

10 (44) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
15 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TCACAATGCT AGGTGTGGTC

20

20 (45) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
25 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGCATAGACA ATGGGATTAC AG

22

30 (46) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 511 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

056730026 050604

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

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5 TGCAACAACT TGAGATCAAA TATGACTTCC TATATGAAAA GGAACACATC TGCTGCTTAG 120  
AAGAGTGGAC CAGCCCTGTG CACCAGAAGA TCTACACCAC CTTCATCCTT GTCATCCTCT 180  
TCCTCCTGCC TCTTATGGTG ATGCTTATTTC TGTACGTAAA ATTGGTTATG AACTTTGGAT 240  
AAAGAAAAGA GTTGGGGATG GTTCAGTGCT TCGAACTATT CATGGAAAAG AAATGTCCAA 300  
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10 TGTGTGCTGG GCACCCATTCC ATGTTGTCCA TATGATGATT GAATACAGTA ATTTTGAAAA 420  
GGAATATGAT GATGTCACAA TCAAGATGAT TTTTGCTATC GTGCAAATTA TTGGATTTTC 480  
CAACTCCATC TGTAATCCCA TTGTCTATGC A 511

(47) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
15 (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTGCTTAGAA GAGTGGACCA G

21

(48) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (iv) ANTI-SENSE: NO

SEQUENCE RECORDS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTGTGCACCA GAAGATCTAC AC

22

(49) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAAGGATGAA GGTGGTGTAG A

21

(50) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTTAGATCT TCTGGTGCAC AGG

23

(51) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAATGCAGG TCATAGTGAG C

21

(52) INFORMATION FOR SEQ ID NO:51:

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- 5                   (i) SEQUENCE CHARACTERISTICS:  
                     (A) LENGTH: 27 base pairs  
                     (B) TYPE: nucleic acid  
                     (C) STRANDEDNESS: single  
                     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

10 TGGAGCATGG TGACGGGAAT GCAGAAG

27

(53) INFORMATION FOR SEQ ID NO:52:

- 15                  (i) SEQUENCE CHARACTERISTICS:  
                     (A) LENGTH: 27 base pairs  
                     (B) TYPE: nucleic acid  
                     (C) STRANDEDNESS: single  
                     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

20 GTGATGAGCA GGTCACTGAG CGCCAAG

27

(54) INFORMATION FOR SEQ ID NO:53:

- 25                  (i) SEQUENCE CHARACTERISTICS:  
                     (A) LENGTH: 23 base pairs  
                     (B) TYPE: nucleic acid  
                     (C) STRANDEDNESS: single  
                     (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

30 GCAATGCAGG CGCTTAACAT TAC

23

(55) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
                     (A) LENGTH: 22 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: DNA (genomic)

5       (iv) ANTI-SENSE: YES

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTGGGTTACA ATCTGAAGGG CA

22

(56) INFORMATION FOR SEQ ID NO:55:

- 10       (i) SEQUENCE CHARACTERISTICS:  
            (A) LENGTH: 23 base pairs  
            (B) TYPE: nucleic acid  
            (C) STRANDEDNESS: single  
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: DNA (genomic)

15       (iv) ANTI-SENSE: NO

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACTCCGTGTC CAGCAGGACT CTG

23

(57) INFORMATION FOR SEQ ID NO:56:

- 20       (i) SEQUENCE CHARACTERISTICS:  
            (A) LENGTH: 24 base pairs  
            (B) TYPE: nucleic acid  
            (C) STRANDEDNESS: single  
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: DNA (genomic)

25       (iv) ANTI-SENSE: YES

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TGCGTGTTCC TGGACCCCTCA CGTG

24

(58) INFORMATION FOR SEQ ID NO:57:

- 30       (i) SEQUENCE CHARACTERISTICS:  
            (A) LENGTH: 29 base pairs  
            (B) TYPE: nucleic acid  
            (C) STRANDEDNESS: single  
            (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CAGGCCTTGG ATTTTAATGT CAGGGATGG

29

5 (59) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGAGAGTCAG CTCTGAAAGA ATTCAAG

27

15 (60) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TGATGTGATG CCAGATACTA ATAGCAC

27

25 (61) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

TRANSGENIC ZEBRAFISH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCTGATTCA TTAGGTGAGA TTGAGAC

27

(62) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GACAGGTACC TTGCCATCAA G

21

(63) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTGCACAATG CCAGTGATAA GG

22

(64) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTGACTTCTT GTTCCTGGCA GCAGCGG

27

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## (65) INFORMATION FOR SEQ ID NO:64:

- 5                   (i) SEQUENCE CHARACTERISTICS:  
                      (A) LENGTH: 27 base pairs  
                      (B) TYPE: nucleic acid  
                      (C) STRANDEDNESS: single  
                      (D) TOPOLOGY: linear  
  
                     (ii) MOLECULE TYPE: DNA (genomic)  
  
                     (iv) ANTI-SENSE: YES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

10 AGACCAGCCA GGGCACCGCTG AAGAGTG

27

## (66) INFORMATION FOR SEQ ID NO:65:

- 15                  (i) SEQUENCE CHARACTERISTICS:  
                      (A) LENGTH: 32 base pairs  
                      (B) TYPE: nucleic acid  
                      (C) STRANDEDNESS: single  
                      (D) TOPOLOGY: linear  
  
                     (ii) MOLECULE TYPE: DNA (genomic)  
  
                     (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

20 GATCAAGCTT CCATCCTACT GAAACCATGG TC

32

## (67) INFORMATION FOR SEQ ID NO:66:

- 25                  (i) SEQUENCE CHARACTERISTICS:  
                      (A) LENGTH: 35 base pairs  
                      (B) TYPE: nucleic acid  
                      (C) STRANDEDNESS: single  
                      (D) TOPOLOGY: linear  
  
                     (ii) MOLECULE TYPE: DNA (genomic)  
  
                     (iv) ANTI-SENSE: YES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

30 GATCAGATCT CAGTTCCAAT ATTACACACCA CCGTC

35

## (68) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTGGTGTGCT CCATGGCATC CC

22

(69) INFORMATION FOR SEQ ID NO:68:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GTAAGCCTCC CAGAACGAGA GG

22

(70) INFORMATION FOR SEQ ID NO:69:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGCGCAGGG TGAAGCCTGA GAGC

24

(71) INFORMATION FOR SEQ ID NO:70:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GGCACCTGCT GTGACCTGTG CAGG

24

5 (72) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GTCCTGCCAC TTCGAGACAT GG

22

15 (73) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GAAACTTCTC TGCCCTTACC GTC

23

25 (74) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

09876076 \* 060604

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

26

CCAACACCAAG CATCCATGGC ATCAAAG

(75) INFORMATION FOR SEQ ID NO:74:

- 5                   (i) SEQUENCE CHARACTERISTICS:  
                      (A) LENGTH: 27 base pairs  
                      (B) TYPE: nucleic acid  
                      (C) STRANDEDNESS: single  
                      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10                 (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

27

GGAGAGTCAG CTCTGAAAGA ATTCAAGG

SEQUENCE LISTING

<110> Chen, Ruoping  
Dang, Huong T.  
Liaw, Chen W.  
Lin, I-Lin

<120> Human Orphan G Protein Coupled Receptors

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Leu Ala Ala Gly Leu Pro Leu Asn Ala Leu Ala Leu Trp Val Phe Leu  
35 40 45

Arg	Ala	Leu	Arg	Val	His	Ser	Val	Val	Ser	Val	Tyr	Met	Cys	Asn	Leu
50							55				60				
Ala	Ala	Ser	Asp	Leu	Leu	Phe	Thr	Leu	Ser	Leu	Pro	Val	Arg	Leu	Ser
65							70			75			80		
Tyr	Tyr	Ala	Leu	His	His	Trp	Pro	Phe	Pro	Asp	Leu	Leu	Cys	Gln	Thr
													85	90	95
Thr	Gly	Ala	Ile	Phe	Gln	Met	Asn	Met	Tyr	Gly	Ser	Cys	Ile	Phe	Leu
													100	105	110
Met	Leu	Ile	Asn	Val	Asp	Arg	Tyr	Ala	Ala	Ile	Val	His	Pro	Leu	Arg
													115	120	125
Leu	Arg	His	Leu	Arg	Arg	Pro	Arg	Val	Ala	Arg	Leu	Leu	Cys	Leu	Gly
													130	135	140
Val	Trp	Ala	Leu	Ile	Leu	Val	Phe	Ala	Val	Pro	Ala	Ala	Arg	Val	His
													145	150	160
Arg	Pro	Ser	Arg	Cys	Arg	Tyr	Arg	Asp	Leu	Glu	Val	Arg	Leu	Cys	Phe
													165	170	175
Glu	Ser	Phe	Ser	Asp	Glu	Leu	Trp	Lys	Gly	Arg	Leu	Leu	Pro	Leu	Val
													180	185	190
Leu	Leu	Ala	Glu	Ala	Leu	Gly	Phe	Leu	Leu	Pro	Leu	Ala	Ala	Val	Val
													195	200	205
Tyr	Ser	Ser	Gly	Arg	Val	Phe	Trp	Thr	Leu	Ala	Arg	Pro	Asp	Ala	Thr
													210	215	220
Gln	Ser	Gln	Arg	Arg	Arg	Lys	Thr	Val	Arg	Leu	Leu	Leu	Ala	Asn	Leu
													225	230	240
Val	Ile	Phe	Leu	Leu	Cys	Phe	Val	Pro	Tyr	Asn	Ser	Thr	Leu	Ala	Val
													245	250	255
Tyr	Gly	Leu	Leu	Arg	Ser	Lys	Leu	Val	Ala	Ala	Ser	Val	Pro	Ala	Arg
													260	265	270
Asp	Arg	Val	Arg	Gly	Val	Leu	Met	Val	Met	Val	Leu	Leu	Ala	Gly	Ala
													275	280	285
Asn	Cys	Val	Leu	Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ala	Glu	Gly	Phe
													290	295	300

Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser  
305 310 315 320

Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala  
325 330 335

Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu  
340 345 350

Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln  
355 360 365

Asp Ser Ala Leu  
370

<210> 5  
<211> 1107

<212> DNA  
<213> Homo sapiens

<400> 5  
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cgcacgcccgg gactgcgcga cgcgctctac ctggcgcacc tttgtgcgttggg ggacctgtcg 180  
ggggccgcctt ccatcatgcc gctgggcctt ctggccgcac cgccgcgggg gctggggccgc 240  
gtgcgcctgg gccccgcgcc atgcccgcgc gctcgcttcc tctccgcgcgc tctgtgcgcg 300  
gcctgcacgc tcgggggtggc cgcaatttggc ctggcacgtt accgcctcat cgtgcaccccg 360  
ctgcggccag gtcgcggcc gcccgcgttg ctcgtgcata cccgcgttg ggccgcggcg 420  
ggactgctgg gcgcgcttc cctgtcgcc cccgcgcggg caccgcgggg tgctccgtgt 480  
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gatagccgcc tttccatctt gcccgcgtc cggcctcgcc tgcccgaaaaaa caaggcggcc 720  
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ggccacccgtt agagttctctt ctccctga 1107

<210> 6  
<211> 368  
<212> PRT  
<213> Homo sapiens

<400> 6

Met Ala Asn Ser Thr Gly Leu Asn Ala Ser Glu Val Ala Gly Ser Leu  
1 5 10 15

Gly Leu Ile Leu Ala Ala Val Val Glu Val Gly Ala Leu Leu Gly Asn  
20 25 30

Gly Ala Leu Leu Val Val Leu Arg Thr Pro Gly Leu Arg Asp Ala  
35 40 45

Leu Tyr Leu Ala His Leu Cys Val Val Asp Leu Leu Ala Ala Ala Ser  
50 55 60

Ile Met Pro Leu Gly Leu Leu Ala Ala Pro Pro Pro Gly Leu Gly Arg  
65 70 75 80

Val Arg Leu Gly Pro Ala Pro Cys Arg Ala Ala Arg Phe Leu Ser Ala  
85 90 95

Ala Leu Leu Pro Ala Cys Thr Leu Gly Val Ala Ala Leu Gly Leu Ala  
100 105 110

Arg Tyr Arg Leu Ile Val His Pro Leu Arg Pro Gly Ser Arg Pro Pro  
115 120 125

Pro Val Leu Val Leu Thr Ala Val Trp Ala Ala Ala Gly Leu Leu Gly  
130 135 140

Ala Leu Ser Leu Leu Gly Pro Pro Pro Ala Pro Pro Pro Ala Pro Ala  
145 150 155 160

Arg Cys Ser Val Leu Ala Gly Gly Leu Gly Pro Phe Arg Pro Leu Trp  
165 170 175

Ala Leu Leu Ala Phe Ala Leu Pro Ala Leu Leu Leu Gly Ala Tyr  
180 185 190

Gly Gly Ile Phe Val Val Ala Arg Arg Ala Ala Leu Arg Pro Pro Arg  
195 200 205

Pro Ala Arg Gly Ser Arg Leu Arg Ser Asp Ser Leu Asp Ser Arg Leu  
210 215 220

Ser Ile Leu Pro Pro Leu Arg Pro Arg Leu Pro Gly Gly Lys Ala Ala  
225 230 235 240

Leu Ala Pro Ala Leu Ala Val Gly Gln Phe Ala Ala Cys Trp Leu Pro  
245 250 255

Tyr Gly Cys Ala Cys Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu  
260 265 270

Ala Ala Val Thr Trp Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe  
275 280 285

Leu Tyr Gly Leu Leu Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu  
290 295 300

Ser Arg Arg Ala Leu Pro Gly Pro Val Arg Ala Cys Thr Pro Gln Ala  
305 310 315 320

Trp His Pro Arg Ala Leu Leu Gln Cys Leu Gln Arg Pro Pro Glu Gly  
325 330 335

Pro Ala Val Gly Pro Ser Glu Ala Pro Glu Gln Thr Pro Glu Leu Ala  
340 345 350

Gly Gly Arg Ser Pro Ala Tyr Gln Gly Pro Pro Glu Ser Ser Leu Ser  
355 360 365

<210> 7  
<211> 1008  
<212> DNA  
<213> Homo sapiens

<400> 7

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actaacacac tagtggtgt ggctgtgctg ctgttgcattcc acaagaatga tgggtgtcagt 120  
ctctgttca ccttgaatct ggctgtggct gacacccatga ttgggtgtggc catctctggc 180  
ctactcacag accagctctc cagcccttct cggcccacac agaagaccct gtgcagccctg 240  
cgatggcat ttgtcaatttc ctccgcagct gcctctgtcc tcacggcat gctgatcacc 300  
tttgacaggt accttgccat caaggcagccc ttccgctact tgaagatcat gagttgggttc 360  
gtggccgggg cctgcattgc cgggctgtgg ttagtgtctt acctcattgg cttccctccca 420  
ctcgaaatcc ccatgttcca gcagactgcc tacaaaggc agtgcagctt ctttgctgtta 480  
tttcacccttc acttcgtgt gaccctctcc tgcgttggt tttccctccagc catgttcctc 540  
tttgtttct tctactgcga catgctcaag attgcctcca tgcacagccca gcagattcga 600  
aagatggAAC atgcaggAGC catggctgga ggttatcgat cccccacggac tcccacggac 660  
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ttcccttatca ctggcattgt gcagggtggcc tgccaggagt gtcacctcta cctagtgctg 780  
gaacggtaCC tggggctgt cggcgtggc aactccctgc tcaacccact catctatgcc 840  
tattggcaga aggaggtgcg actgcagctc taccacatgg cccttaggat gaagaagggtg 900  
ctcacctcat tcctcctt tctctcgccc aggaattgtg gcccagagag gcccaggaa 960

agttcctgtc acatcgac tatctccagc tcagagtttgc atggctaa

1008

<210> 8

<211> 335

<212> PRT

<213> Homo sapiens

<400> 8

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser  
1 5 10 15

Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu  
20 25 30

Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala  
35 40 45

Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp  
50 55 60

Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu  
65 70 75 80

Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val  
85 90 95

Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg  
100 105 110

Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly  
115 120 125

Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro  
130 135 140

Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val  
145 150 155 160

Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro  
165 170 175

Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala  
180 185 190

Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met  
195 200 205

Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu  
210 215 220

Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro  
225 230 235 240

Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu  
245 250 255

Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser  
260 265 270

Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gin Lys Glu Val Arg Leu  
275 280 285

Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe  
290 295 300

Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu  
305 310 315 320

Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly  
325 330 335

<210> 9

<211> 1413

<212> DNA

<213> Homo sapiens

<400> 9

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ctccttgggc tgccagccaa tgggttgatg gcgtggctgg ccggctccca ggcccgcat 180  
ggagctggca cgcgcttggc gctgctcctg ctcagcctgg ccctctctga cttcttggtc 240  
ctggcagcag cggccttcca gatccttagag atccggcatg ggggacactg gccgctgggg 300  
acagctgcct gccgcttcta ctacttccta tggggcgtgt cctactccctc cggccttcc 360  
ctgctggccg ccctcagcct cgaccgctgc ctgctggcgc tgtgcccaca ctggtaccct 420  
gggcacccgcc cagtccgcct gcccctctgg gtctgcgcgg gtgtctgggt gctggccaca 480  
ctcttcagcg tgccctggct ggtcttcccc gaggtgcgg tctggtgta cgacctggtc 540  
atctgcctgg acttctggga cagcgaggag ctgtcgctga ggatgctgga ggtcttgggg 600  
ggcttcctgc ctttcctcct gctgctcgcc tgccacgtgc tcaccaggc cacagcctgt 660  
cgcacctgcc accgccaaca gcagccccca gcctgccccgg gcttcgcggc tgtggccagg 720  
accattctgt cagcctatgt gtcctgagg ctgccttacc agctggccca gctgtctac 780  
ctggccttcc tggggacgt ctactctggc tacctgctct gggaggccct ggtctactcc 840  
gactacctga tcctactcaa cagctgcctc agcccttcc tctgcctcat ggccagtgcc 900  
gacctccgga ccctgctgcg ctccgtgc tcgtccttcg cggcagctct ctgcgaggag 960  
cggccggca gcttcacgca cactgagcca cagacccagc tagattctga gggtccaact 1020

ctgccagacg cgatggcaga ggcccagtca cagatggatc ctgtggcca gcctcagg 1080  
aaccccacac tccagccacg atcggatccc acagctcagc cacagctgaa ccctacggcc 1140  
cagccacagt cggatccac agcccagcca cagctgaacc tcataggcca gccacagtca 1200  
gattctgtgg cccagccaca ggcagacact aacgtccaga cccctgcacc tgctgccagt 1260  
tctgtgcccgttcc gtcctgtga tgaagcttcc ccaacccat cctcgcatcc tacccagg 1320  
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ccagaggcgg ccccgccgc aggccccacg tga 1413

<210> 10  
<211> 468  
<212> PRT  
<213> Homo sapiens

<400> 10  
Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro  
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Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp  
20 25 30  
  
Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly  
35 40 45  
  
Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr  
50 55 60  
  
Arg Leu Ala Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe  
65 70 75 80  
  
Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His  
85 90 95  
  
Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly  
100 105 110  
  
Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Leu Ser Leu Asp  
115 120 125  
  
Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro  
130 135 140  
  
Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr  
145 150 155 160  
  
Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp  
165 170 175

Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser  
 180 185 190  
  
 Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu  
 195 200 205  
  
 Leu Val Cys His Val Leu Thr Gln Ala Thr Arg Thr Cys His Arg Gln  
 210 215 220  
  
 Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile  
 225 230 235 240  
  
 Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu  
 245 250 255  
  
 Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp  
 260 265 270  
  
 Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu  
 275 280 285  
  
 Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu  
 290 295 300  
  
 Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro  
 305 310 315 320  
  
 Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly  
 325 330 335  
  
 Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro  
 340 345 350  
  
 Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro  
 355 360 365  
  
 Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro  
 370 375 380  
  
 Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser  
 385 390 395 400  
  
 Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala  
 405 410 415  
  
 Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala Ser Pro Thr Pro Ser  
 420 425 430

Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro Ala Thr Pro Pro Ala  
435 440 445

Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro Glu Ala Ala Pro Gly  
450 455 460

Ala Gly Pro Thr  
465

<210> 11  
<211> 1248  
<212> DNA  
<213> Homo sapiens

<400> 11

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cgcagccact ttttcctccc cgtgtctgt gtgtatgtgc caattttgtt ggtgggggtc 180  
atggcaatg tcctggatgt cctggtgatt ctgcagcacc aggctatgaa gacgccccacc 240  
aactactacc ttttcagcct ggccgtctct gacccctgg tcctgctcct tggaatgccc 300  
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aacaccagca tccatggcat caagttccac tactttccca atgggtccctt ggtcccagg 600  
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tggggccctt tccacattta cccacttttcc ttcatgtt tggaggagtg gatgtatcc 900  
ctggctgtgt tggtcaaccc cgtccatgt gtgtcagggt ttttttttca ccttagtca 960  
gctgtcaacc ccattatcta taacctactg tctccggct tccaggcagc attccagaat 1020  
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caatttttttcat gtcagtcatc catgcacaac tctcacctcc caacagccctt ctctgtt 1200  
cagatgtcaa gaacaaacta tcaaagtttcc cacttttaca aaacctga 1248

<210> 12  
<211> 415  
<212> PRT  
<213> Homo sapiens

<400> 12

Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln  
1 5 10 15



Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg  
275 280 285

Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val  
290 295 300

Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser  
305 310 315 320

Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala  
325 330 335

Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln  
340 345 350

His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu  
355 360 365

Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys  
370 375 380

Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu  
385 390 395 400

Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr  
405 410 415

<210> 13

<211> 1173

<212> DNA

<213> Homo sapiens

<400> 13

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gtgggtggaca aaaaccttag acatcgaagt agttatttt ttcttaactt ggccatctct 180  
gacttctttg tgggtgtgat ctccattcct ttgtacatcc ctcacacgct gttcgaatgg 240  
gattttggaa aggaaatctg tgtattttg ctcactactg actatctgtt atgtacagca 300  
tctgtatata acattgtcct catcagctat gatcgatacc tgtcagtctc aaatgctgtg 360  
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tccaaacatct gtggacactc attcagaggt agactatctt caaggagatc tctttctgca 720  
tcgacagaag ttcctgcattc ctttcatca gagagacaga ggagaaaagag tagtctcatg 780  
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caatcagatt ctgttagctct tcaccaaagg gaacatgttg aactgcttag agccaggaga 900  
ttagccaagt cactggccat tctcttaggg gttttgctg tttgctggc tccatattct 960  
ctgttcacaa ttgtcctttc attttattcc tcagcaacag gtcctaaatc agtttggtat 1020  
agaattgcat tttggcttca gtgggtcaat tccttgtca atcctctttt gtatccattg 1080  
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ccatcacaac acagtcggtc agtatcttct taa 1173

<210> 14  
<211> 390  
<212> PRT  
<213> Homo sapiens

<400> 14  
Met Pro Asp Thr Asn Ser Thr Ile Asn Leu Ser Leu Ser Thr Arg Val  
1 5 10 15  
  
Thr Leu Ala Phe Phe Met Ser Leu Val Ala Phe Ala Ile Met Leu Gly  
20 25 30  
  
Asn Ala Leu Val Ile Leu Ala Phe Val Val Asp Lys Asn Leu Arg His  
35 40 45  
  
Arg Ser Ser Tyr Phe Phe Leu Asn Leu Ala Ile Ser Asp Phe Phe Val  
50 55 60  
  
Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe Glu Trp  
65 70 75 80  
  
Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp Tyr Leu  
85 90 95  
  
Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr Asp Arg  
100 105 110  
  
Tyr Leu Ser Val Ser Asn Ala Val Ser Tyr Arg Thr Gln His Thr Gly  
115 120 125  
  
Val Leu Lys Ile Val Thr Leu Met Val Ala Val Trp Val Leu Ala Phe  
130 135 140  
  
Leu Val Asn Gly Pro Met Ile Leu Val Ser Glu Ser Trp Lys Asp Glu  
145 150 155 160  
  
Gly Ser Glu Cys Glu Pro Gly Phe Phe Ser Glu Trp Tyr Ile Leu Ala  
165 170 175  
  
Ile Thr Ser Phe Leu Glu Phe Val Ile Pro Val Ile Leu Val Ala Tyr

180 185 190

Phe Asn Met Asn Ile Tyr Trp Ser Leu Trp Lys Arg Asp His Leu Ser  
195 200 205

Arg Cys Gln Ser His Pro Gly Leu Thr Ala Val Ser Ser Asn Ile Cys  
210 215 220

Gly His Ser Phe Arg Gly Arg Leu Ser Ser Arg Arg Ser Leu Ser Ala  
225 230 235 240

Ser Thr Glu Val Pro Ala Ser Phe His Ser Glu Arg Gln Arg Arg Lys  
245 250 255

Ser Ser Leu Met Phe Ser Ser Arg Thr Lys Met Asn Ser Asn Thr Ile  
260 265 270

Ala Ser Lys Met Gly Ser Phe Ser Gln Ser Asp Ser Val Ala Leu His  
275 280 285

Gln Arg Glu His Val Glu Leu Leu Arg Ala Arg Arg Leu Ala Lys Ser  
290 295 300

Leu Ala Ile Leu Leu Gly Val Phe Ala Val Cys Trp Ala Pro Tyr Ser  
305 310 315 320

Leu Phe Thr Ile Val Leu Ser Phe Tyr Ser Ser Ala Thr Gly Pro Lys  
325 330 335

Ser Val Trp Tyr Arg Ile Ala Phe Trp Leu Gln Trp Phe Asn Ser Phe  
340 345 350

Val Asn Pro Leu Leu Tyr Pro Leu Cys His Lys Arg Phe Gln Lys Ala  
355 360 365

Phe Leu Lys Ile Phe Cys Ile Lys Lys Gln Pro Leu Pro Ser Gln His  
370 375 380

Ser Arg Ser Val Ser Ser  
385 390

<210> 15  
<211> 1128  
<212> DNA  
<213> Homo sapiens

<400> 15

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ctgctgatcg tgcgggagcg cagcctgcac cgcgcggcg actacactgct gctgacactg 180  
tgcctggccg acgggctgcg cgcgcgcgc tgccctccgg ccgtcatgct ggcggcgccg 240  
cgtgcggcgcc cgccggcgccg ggccgcgcgg gctgcaagct gctgccttc 300  
ctggccgcgc tcttctgctt ccacgcgcgc ttctctgctc tggcgtggg cgtcaccgc 360  
tacctggcca tcgcgcacca cgcgttat gcagagcgc tggccggctg gccgtgcgc 420  
gccatgctgg tgtgcgcgc ctggcgctg ggcgtggccg ccgccttc gccagtgc 480  
gacggcggtg ggcacgacga ggacgcgcgg tgccgcctgg agcagcggcc cgacggcgcc 540  
ccggcgccgc tggcgttctt gctgctgctg ggcgtgggtg tggcgcac gcacctgc 600  
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cccgccgtca gccacgactg gaccccttccac ggcccggcg ccaccggcca ggccggcc 720  
aactggacgg cgggcttcgg cgcggggccc acgcccggc cgcttgcgttgg catccggccc 780  
gcagggccgg ggcgcggcgc ggcgcgcctc ctgcgtgtgg aagaattcaa gacggagaag 840  
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gtcgtggcca gctacctgcg gtcctgttg cggccggcg ccgtccccca ggcctacctg 960  
acggccctccg tgtggctgac ctgcgcgcag gccggcatca accccgtcgt gtgccttc 1020  
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<210> 16

<211> 375

<212> PRT

<213> Homo sapiens

<400> 16

Met Ala Asn Ala Ser Glu Pro Gly Gly Ser Gly Gly Gly Glu Ala Ala  
1 5 10 15

Ala Leu Gly Leu Lys Leu Ala Thr Leu Ser Leu Leu Leu Cys Val Ser  
20 25 30

Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser  
35 40 45

Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp  
50 55 60

Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg  
65 70 75 80

Arg Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys  
85 90 95

Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu  
100 105 110

Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg  
115 120 125

Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val  
130 135 140

Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Ala Phe Pro Pro Val Leu  
145 150 155 160

Asp Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg  
165 170 175

Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Ala Val  
180 185 190

Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile  
195 200 205

His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser  
210 215 220

His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala Ala Ala  
225 230 235 240

Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val  
245 250 255

Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val  
260 265 270

Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala  
275 280 285

Val Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val Ala Ser  
290 295 300

Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu  
305 310 315 320

Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn Pro Val  
325 330 335

Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln  
340 345 350

Phe Pro Cys Cys Gln Ser Pro Arg Thr Thr Gln Ala Thr His Pro Cys  
355 360 365

Asp Leu Lys Gly Ile Gly Leu  
370 375

<210> 17  
<211> 1002  
<212> DNA  
<213> Homo sapiens

<400> 17  
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atagtacagc tggattccc agccctctac acagtggttt tcttgaccgg catcctgctg 120  
aatactttgg ctctgtgggt gtttggcac atccccagct cctccacctt catcatctac 180  
ctcaaaaaca ctttggcgc cgacttgata atgacactca tgcttcctt caaaatcctc 240  
tctgactcac acctgcacc ctggcagctc agagctttg tgtgtcggtt ttcttcgg 300  
atattttatg agaccatgta tggggcattc gtgctgttag ggctcatagc ctttgacaga 360  
ttcctaaga tcatacggacc ttggagaaat attttctaa aaaaacctgt ttttgaaaaa 420  
acggtctcaa tcttcatctg gttcttttgc ttcttcatct ccctgcca 480  
agcaacaagg aagcaacacc atcgtctgtg aaaaagtgtg cttccattaa ggggcctctg 540  
gggctgaaat ggcataaat ggtaaataac atatgccagt ttatttctg gactgtttt 600  
atccataatgc ttgtgttttgc ttgtgttatt gcaaaaaaag tatatgattc ttatagaaag 660  
tccaaaagta aggacagaaa aaacaacaaa aagctggaaag gcaaaagtatt ttgtgtcg 720  
gttgtcttct ttgtgtgtt tgctccattt cattttggca gagttccata tactcacagt 780  
caaaccacaa ataagactga ctgttagactg caaaatcaac tgtttattgc taaagaaaaca 840  
actctctttt tggcagcaac taacatttg atggatccct taatatacat attcttatgt 900  
aaaaaattca cagaaaaagct accatgtatg caagggagaa agaccacagc atcaagccaa 960  
gaaaatcata gcagtcagac agacaacata accttaggct ga 1002

<210> 18  
<211> 333  
<212> PRT  
<213> Homo sapiens

<400> 18  
Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro  
1 5 10 15

Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val  
20 25 30

Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe  
35 40 45

Val His Ile Pro Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr  
50 55 60

Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu

65	70	75	80
Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg			
85	90	95	
Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu			
100	105	110	
Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu			
115	120	125	
Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile			
130	135	140	
Phe Ile Trp Phe Phe Leu Phe Ile Ser Leu Pro Asn Thr Ile Leu			
145	150	155	160
Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu			
165	170	175	
Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys			
180	185	190	
Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val			
195	200	205	
Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys			
210	215	220	
Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val			
225	230	235	240
Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro			
245	250	255	
Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn			
260	265	270	
Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn			
275	280	285	
Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr			
290	295	300	
Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln			
305	310	315	320
Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly			

325

330

<210> 19  
<211> 1122  
<212> DNA  
<213> Homo sapiens

<400> 19  
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gccatcttgt ccctgctggt gctcaaggag cgtgccctgc acaaggctcc ttactacttc 180  
ctgctggacc tgtgcctggc cgatggata cgctctgccc tctgcttccc ttgtgtgctg 240  
gcttctgtgc gccacggctc ttcatggacc ttca gtc ac tc agctgcaa gattgtggcc 300  
tttatggccg tgctctttg ctccatgcg gccttcatgc ttttgc cat cagcgtcacc 360  
cgctacatgg ccatacgccca ccaccgcttc ta gcca agc gcatgacact ctggacatgc 420  
gcggctgtca tctgcatggc ctggaccctg tctgtggcca tggccttccc acctgtctt 480  
gacgtggca cctacaagtt tattcgggag gaggaccagt gcatcttga gcatcgctac 540  
ttcaaggcca atgacacgct gggcttcatg ctatgttgg ctgtgctcat ggcagctacc 600  
catgctgtct acggcaagct gctccttgc gagtatcgac accgcaagat gaagccagtg 660  
cagatggtgc cagccatcag ccagaactgg acattccatg gtcccgggc caccggccag 720  
gctgctgcca actggatcgc cggcttggc cgtggccca tgccaccaac cctgctgggt 780  
atccggcaga atggcatgc agccagccgg cggctactgg gcatggacga ggtcaagggt 840  
aaaaagcagc tggccgcat gttctacgcg atcacactgc tctttctgct cctctggtca 900  
ccctacatcg tggcctgcta ctggcgagtg ttgtgaaag cctgtgctgt gccccaccgc 960  
tacctggcca ctgctgtttg gatgagctc gcccaggctg ccgtcaaccc aattgtctgc 1020  
ttcctgctca acaaggacct caagaagtgc ctgaccactc acgccccctg ctggggcaca 1080  
ggaggtgccc cgctccca agaaccc tac t g t g t c a t g t g a 1122

<210> 20  
<211> 373  
<212> PRT  
<213> *Homo sapiens*

<400> 20  
Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser  
1 5 10 15

Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile  
 20 25 30

Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu  
35 40 45

Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu  
50 55 60

Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu  
65 70 75 80

Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys  
85 90 95

Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe  
100 105 110

Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His  
115 120 125

Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile  
130 135 140

Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe  
145 150 155 160

Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe  
165 170 175

Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met  
180 185 190

Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu  
195 200 205

Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro  
210 215 220

Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln  
225 230 235 240

Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro  
245 250 255

Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu  
260 265 270

Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe  
275 280 285

Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val  
290 295 300

Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg  
305 310 315 320

Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn  
325 330 335

Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Thr  
340 345 350

Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu  
355 360 365

Pro Tyr Cys Val Met  
370

<210> 21  
<211> 1053  
<212> DNA  
<213> Homo sapiens

<400> 21  
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aaagtttcc tccctgtatt cctcacaata gctttcgta ttggacttgc aggcaattcc 180  
atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240  
ctgaatttgg ctgttagcaga tttactcctt ctattcactc tgccttttg ggctgttaat 300  
gcagttcatg ggtgggtttt agggaaaata atgtcaaaa taacttcaggc cttgtacaca 360  
ctaaacttttgc tctctggaat gcagttctg gcttgcata gcatagacag atatgtggca 420  
gtaaactaatg tccccagcca atcaggagtg ggaaaaccat gctggatcat ctgtttctgt 480  
gtctggatgg ctgccatctt gctgagcata ccccaactgg ttttttatac agtaaatgac 540  
aatgcttaggt gcattccat tttccccgc tacctaggaa catcaatgaa agcattgatt 600  
caaatgctag agatctgcat tggatttcta gtacccttc ttattatggg ggtgtgctac 660  
tttatcacgg caaggacact catgaagatg ccaaacatta aaatatctcg acccctaaaa 720  
gttctgctca cagtcgttat agttttcatt gtcactcaac tgccttataa cattgtcaag 780  
ttctgccgag ccatagacat catctactcc ctgatcacca gctgcaacat gagcaaacgc 840  
atggacatcg ccatccaagt cacagaaagc attgcactct ttcacagctg cctcaaccca 900  
atcccttatg ttttatggg agcatcttc aaaaactacg ttatgaaagt ggccaagaaaa 960  
tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttcctttga ttctgagggt 1020  
cctacagagc caaccagtac ttttagcatt taa 1053

<210> 22  
<211> 350  
<212> PRT  
<213> Homo sapiens

<400> 22  
Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn  
1 5 10 15

Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile  
20 25 30

Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu  
35 40 45

Thr Ile Ala Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala  
50 55 60

Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile  
65 70 75 80

Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Phe Thr Leu Pro Phe  
85 90 95

Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys  
100 105 110

Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln  
115 120 125

Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Asn Val  
130 135 140

Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys  
145 150 155 160

Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr  
165 170 175

Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu  
180 185 190

Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly  
195 200 205

Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala  
210 215 220

Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys  
225 230 235 240

Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr  
245 250 255

Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile  
260 265 270

Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr  
275 280 285

Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val  
290 295 300

Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys  
305 310 315 320

Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe  
325 330 335

Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile  
340 345 350

<210> 23

<211> 1116

<212> DNA

<213> Homo sapiens

<400> 23

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agcgcggtgt gcacgcgtggg ggtgcgggccc aactgcctga ctgcgtggc ggcgtgctg 180  
caggtactgc agggcaacgt gctggccgtc tacctgctct gcctggcact ctgcgaactg 240  
ctgtacacag gcacgcgtgcc actctgggtc atctatatcc gcaaccagca ccgcgtggacc 300  
ctaggcctgc tggcctcgaa ggtgaccggcc tacatcttct tctgcaacat ctacgtcagc 360  
atccctttcc tgtgctgcat ctcctgcgac cgcttcgtgg ccgtggtgta cgcgtggag 420  
agtccggggcc gccgcccgcg gaggaccgcctt atcctcatct ccgcctgcattt cttcatcctc 480  
gtcgggatcg ttcaactaccc ggtgttccag acggaagaca aggagacatg ctttgacatg 540  
ctgcagatgg acagcaggat tgccgggtac tactacgcca gtttcaccgt tggctttgcc 600  
atccctctct ccatcatcgc cttcaccaac caccggattt tcaggagcat caagcagagc 660  
atgggcttaa gcgctgcccga gaaggccaag gtgaagcact cggccatcgc ggtgggtgtc 720  
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tcctactaca gaggagacag gaacgcccattt tgccggttgg agggaaaggct gtacacagcc 840  
tctgtgggtgt ttctgtgcct gtccacgggtg aacggcgtgg ctgaccat tatctacgtg 900  
ctggccacgg accattcccg ccaagaagtg tccagaatcc ataagggggtg gaaagagtgg 960  
tccatgaaga cagacgtcac caggctcacc cacagcaggg acaccggaga gctgcagtcg 1020  
cccggtggccc ttgcagacca ctacacccattt tccaggcccg tgcacccacc agggtcacca 1080  
tgccctgcaa agaggctgat tgaggagtcc tgctga 1116

<210> 24

<211> 371

<212> PRT

<213> Homo sapiens

<400> 24  
 Met Pro Gly Asn Ala Thr Pro Val Thr Thr Ala Pro Trp Ala Ser  
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 Leu Gly Leu Ser Ala Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser  
 20 25 30  
  
 Arg Ile Val Leu Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val  
 35 40 45  
  
 Pro Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Gln Val Leu Gln  
 50 55 60  
  
 Gly Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu  
 65 70 75 80  
  
 Leu Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln  
 85 90 95  
  
 His Arg Trp Thr Leu Gly Leu Leu Ala Ser Lys Val Thr Ala Tyr Ile  
 100 105 110  
  
 Phe Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser  
 115 120 125  
  
 Cys Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg  
 130 135 140  
  
 Arg Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu  
 145 150 155 160  
  
 Val Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr  
 165 170 175  
  
 Cys Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr  
 180 185 190  
  
 Ala Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe  
 195 200 205  
  
 Thr Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser  
 210 215 220  
  
 Ala Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val  
 225 230 235 240  
  
 Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys  
 245 250 255

Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly  
260 265 270

Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser  
275 280 285

Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp  
290 295 300

His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp  
305 310 315 320

Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu  
325 330 335

Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg  
340 345 350

Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu  
355 360 365

Glu Ser Cys  
370

<210> 25  
<211> 1113  
<212> DNA  
<213> Homo sapiens

<400> 25

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tttctgaaac tgacttc当地 ggtttcata ataggagtca gcgtggt当地 caacccctg 120  
atctccattt tgcttagtgaa agataagacc ttgc当地 gagacttacta cttccctgtt当地 180  
gatctttgct gttc当地 gagatct cctc当地 gagatct gcaattt当地 tcccatttgtt gttcaactct 240  
gtcaaaaatg gctctacctg gacttatggg actctgactt gcaaaggat gat tgc当地 ttctg 300  
ggggttt当地 ct当地 gtttcca cactgcttcc atgctcttct gcatc当地 gt当地 caccagatac 360  
tttagctatcg cccatcaccg cttctataca aagaggctga cttttggac gtgtctggct 420  
gtgatctgta tgggtggac tctgtctgtg gccatggcat ttccccggc当地 tttagacgtg 480  
ggcacttact cattcattag ggaggaagat caatgc当地 tccaa当地 accgg ctc当地 ct当地 cagg 540  
gctaattgatt ctttaggatt tatgctgctt cttgc当地 tctca tc当地 ct当地 tagc cacacagctt 600  
gtctacctca agctgatatt ttgc当地 tccac gatc当地 aagaa aaatgaaagcc agtccagttt 660  
gtagcagcag tc当地 agccagaa ctggactttt catggctctg gagccagtg ccaggcagct 720  
gccaattggc tagcaggatt tggaaaggggc当地 cccacaccac ccacctt当地 gggcatcagg 780  
caaatgcaa acaccacagg cagaagaagg ctatggct tagacgaggta caaatggag 840  
aaaagaatca gcagaatgtt ctatataatg actttctgt ttctaacctt gtggggcccc 900  
tacctgggtgg cctgttattg gagagttttt gcaagaggc当地 ctgttagtacc agggggattt 960

ctaacagctg ctgtctggat gagtttgcc caaggcggaa tcaatcctt tgtctgcatt 1020  
ttctcaaaca gggagctgag gcgcgtttc agcacaaccc ttctttactg cagaaaatcc 1080  
aggttaccaa gggAACCTTA ctgtgtata tga 1113

<210> 26  
<211> 370  
<212> PRT  
<213> Homo sapiens

<400> 26  
Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser  
1 5 10 15

Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly  
20 25 30

Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp  
35 40 45

Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys  
50 55 60

Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser  
65 70 75 80

Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val  
85 90 95

Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu  
100 105 110

Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe  
115 120 125

Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met  
130 135 140

Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val  
145 150 155 160

Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His  
165 170 175

Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Ala  
180 185 190

Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe

195

200

205

Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val  
210 215 220

Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala  
225 230 235 240

Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu  
245 250 255

Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu  
260 265 270

Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr  
275 280 285

Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala  
290 295 300

Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe  
305 310 315 320

Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro  
325 330 335

Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr  
340 345 350

Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys  
355 360 365

Val Ile  
370

<210> 27

<211> 1080

<212> DNA

<213> Homo sapiens

<400> 27

atgcagggtcc cgaacagcac cggcccgac aacgcgacgc tgcagatgtc gcggaaacctcg 60  
gcgcgcgcgg tggccctgcc cgtggtgtac tcgctgggtgg cggcggtca gatcccgggc 120  
aacctttct ctctgtgggt gctgtgccgg cgcatggggc ccagatcccc gtcgtcatc 180  
ttcatgtatca acctgagcgt cacggacctg atgctggcca gcgtgttgc tttccaaatc 240  
tactaccatt gcaaccgcca ccactgggtta ttcgggggtgc tgctttgcaa cgtggtgacc 300  
gtggccctttt acgcaaacat gtattccagc atcctcacca tgacctgtat cagcgtggag 360

cgcttcctgg gggcctgtta cccgctcagc tccaagcgct ggccgcgcgc tcgttacgcg 420  
gtggccgcgt gtgcagggac ctggctgctg ctcctgaccg ccctgtgccccc gctggcgccgc 480  
accgatctca cctaccgggt gcacgcccctg ggcatcatca cctgcttcga cgtcctcaag 540  
tggacgatgc tccccagcgt ggccatgtgg gccgtgttcc tcttcaccat cttcatcctg 600  
ctgttcctca tcccgttcgt gatcaccgtg gcttggata cggccaccat cctcaagctg 660  
ttgcgcacgg aggaggcgca cggccgggag cagcggaggc gcgccgtggg cctggccgcg 720  
gtggccttgc tggccttgc cacctgctc gcccccaaca acttcgtgct cctggcgac 780  
atcgtgagcc gcctgttcta cgccaagagc tactaccacg tgtacaagct cacgctgtgt 840  
ctcagctgcc tcaacaactg tctggaccacg tttgtttatt actttgcgtc ccggaaattc 900  
cagctgcgcc tgcgggata tttgggctgc cggccgggtgc ccagagacac cctggacacg 960  
cgccgcgaga gcctttctc cgccaggacc acgtccgtgc gctccgaggc cggtgcgcac 1020  
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<210> 28  
<211> 359  
<212> PRT  
<213> Homo sapiens

<400> 28  
Met Gln Val Pro Asn Ser Thr Gly Pro Asp Asn Ala Thr Leu Gln Met  
1 5 10 15  
  
Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu  
20 25 30  
  
Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu  
35 40 45  
  
Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn  
50 55 60  
  
Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile  
65 70 75 80  
  
Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys  
85 90 95  
  
Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu  
100 105 110  
  
Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro  
115 120 125  
  
Leu Ser Ser Lys Arg Trp Arg Arg Arg Tyr Ala Val Ala Ala Cys  
130 135 140  
  
Ala Gly Thr Trp Leu Leu Leu Thr Ala Leu Cys Pro Leu Ala Arg

145	150	155	160
Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe			
165		170	175
Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val			
180	185		190
Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile			
195	200		205
Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu			
210	215		220
Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala			
225	230		235
Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val			
245		250	255
Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr			
260	265		270
His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu			
275	280		285
Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu			
290	295		300
Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr			
305	310		315
Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu			
325	330		335
Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu			
340	345		350
Gln Arg Gln Glu Ser Val Phe			
355			

<210> 29  
<211> 1503  
<212> DNA  
<213> Homo sapiens

<400> 29

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 ccagtgcggc ccggggcgcg ctccggtgcc gcggcgagtg gcacaggctg gcagccatgg 120  
 gctgagtgcc cgggacccaa ggggaggggg caactgctgg cgaccgccc cccttgcgt 180  
 cgctggcccg cccccctcgcc tgccagctcc agccccgccc ccggagcggc gtccgctcac 240  
 tcggttcaag gcagcgac tgcggtggc gcacgaccag ggcgcagacc ttggggcgcg 300  
 cgccccatgg agtcgggct getgcggccg gcgcggtaa gcgaggcat cgtcctgcat 360  
 tacaactaca ccggcaagct ccgcggtgcc agtaccagc cgggtgccc cctgcgcgccc 420  
 gacgcgtgg tgtgcctggc ggtgtgcgc ttcatgtgc tagagaatct agccgtttg 480  
 ttggtgctcg gacgccaccc gcgccttccac gctccatgt tcctgctctt gggcagccctc 540  
 acgttgtcgg atctgtggc aggccgcgac tacgcgcaca acatccact gtcggggccg 600  
 ctcacgctga aactgtcccc cgcgcgttgg ccgcacggg agggaggcgt cttcggtggca 660  
 ctcactgcgt ccgtgcgtgag ctcctggcc atgcgcgttgg agcgcagcctt caccatggcg 720  
 cgccaggggc ccgcgcgtt ctccagtcgg gggcgcacgc tggcgatggc agccgcggcc 780  
 tggggcgtgt cgctgcctt cgggcgttgg ccagcgctgg gctggaaattt cctgggtcgc 840  
 ctggacgcgtt gctccactgt cttgcgcgtc tacgcacaagg cctacgtgt cttctgcgt 900  
 ctcgccttcg tgggcatttgc ggccgcgatc tggcactt acgcgcgtt cttactgcag 960  
 gtacgcgcaca acgcgcggcg cctgcgggca cggccggga ctgcggggac cacctcgacc 1020  
 cggcgcgtc gcaaggcccg ctctctggcc ttgctgcgc cgcgcgttgg ggtgcctctg 1080  
 gcctttgtgg catgttgggg ccccttgc cttgcgtgt tgctgcgtt ggcgtgccc 1140  
 ggcgcacact gtcctgtact cctgcaggcc gatcccttcc tggactgac cttactgcac 1200  
 tcacttctga accccatcat ctacacgcgtt accaaccgcg acctgcgcaca cgcgcctctg 1260  
 cgcctggtct gtcggacgc ccactcctgc ggcagagacc ctagtggcgc ccagcagtcg 1320  
 gcgagcgcgg ctgaggctt cgggggcctg cggcgttgc tggcccccggg cttgtatggg 1380  
 agttcagcg gtcggagcg ctcatgcggc cagcgcgttgc ggctggacac cagcggctcc 1440  
 acaggcagcc cgggtgcacc cacagccgc cggacttgc tatcagaacc ggctgcagac 1500  
 tga 1503

<210> 30  
 <211> 500  
 <212> PRT  
 <213> Homo sapiens

<400> 30  
 Met Glu Arg Pro Trp Glu Asp Ser Pro Pro Gly Pro Glu Gly Ala Ala Glu  
 1 5 10 15

Gly Ser Pro Val Pro Val Ala Ala Gly Ala Arg Ser Gly Ala Ala Ala  
 20 25 30

Ser Gly Thr Gly Trp Gln Pro Trp Ala Glu Cys Pro Gly Pro Lys Gly  
 35 40 45

Arg Gly Gln Leu Leu Ala Thr Ala Gly Pro Leu Arg Arg Trp Pro Ala  
 50 55 60

Pro Ser Pro Ala Ser Ser Ser Pro Ala Pro Gly Ala Ala Ser Ala His  
 65 70 75 80

Ser Val Gln Gly Ser Ala Thr Ala Gly Gly Ala Arg Pro Gly Arg Arg  
85 90 95

Pro Trp Gly Ala Arg Pro Met Glu Ser Gly Leu Leu Arg Pro Ala Pro  
100 105 110

Val Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg  
115 120 125

Gly Ala Ser Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp Ala Val Val  
130 135 140

Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu Ala Val Leu  
145 150 155 160

Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met Phe Leu Leu  
165 170 175

Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala  
180 185 190

Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala  
195 200 205

Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu Thr Ala Ser  
210 215 220

Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu Thr Met Ala  
225 230 235 240

Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr Leu Ala Met  
245 250 255

Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Gly Leu Leu Pro Ala  
260 265 270

Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser Thr Val Leu  
275 280 285

Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu Ala Phe Val  
290 295 300

Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln  
305 310 315 320

Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly  
325 330 335

Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu  
 340 345 350

Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro  
 355 360 365

Leu Phe Leu Leu Leu Leu Asp Val Ala Cys Pro Ala Arg Thr Cys  
 370 375 380

Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn  
 385 390 395 400

Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg  
 405 410 415

His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg  
 420 425 430

Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly  
 435 440 445

Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly  
 450 455 460

Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser  
 465 470 475 480

Thr Gly Ser Pro Gly Ala Pro Thr Ala Ala Arg Thr Leu Val Ser Glu  
 485 490 495

Pro Ala Ala Asp  
 500

<210> 31  
 <211> 1029  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
 atgcaagccg tcgacaatct cacctctgcg cctggaaaca ccagtctgtg caccagagac 60  
 tacaaaatca cccaggtcct cttcccactg ctctacactg tcctgtttt tggactt 120  
 attcacaaatg gcctggcgat gaggatttc ttcaaatacc ggagtaaatc aaaccttatt 180  
 attttctta agaacacagt catttctgtat cttctcatga ttctgacttt tccattcaaa 240  
 attcttagtg atgcacaaact gggAACAGGA ccactgagaa ctttgtgtg tcaagttacc 300  
 tccgtcataat ttatattcac aatgttatatc agtatttcat tcctggact gataactatc 360  
 gatcgctacc agaagaccac caggccattt aaaacatcca accccaaaaa tctcttgggg 420

gctaagattc tctctgttgt catctggca ttcatgttct tactctctt gcctaacatg 480  
attctgacca acaggcagcc gagagacaag aatgtgaaga aatgctctt ccttaaatca 540  
gagttcggtc tagtctggca tgaaatagta aattacatct gtcaagtcat tttctggatt 600  
aatttcttaa ttgttattgt atgttataca ctcattacaa aagaactgta ccggtcatac 660  
gtaagaacga ggggtgttagg taaagtccc aggaaaaagg tgaacgtcaa agtttcatt 720  
atcattgctg tattcttat ttgtttgtt ccttccatt ttgcccgaat tccttacacc 780  
ctgagccaaa cccggatgt ctggactgc actgctgaaa atactctgtt ctatgtgaaa 840  
gagagcactc tgtggtaac ttcccttaat gcatgcctgg atccgttcat ctatttttc 900  
cttgcaagt cttcagaaa ttcccttgata agtatgctga agtgccccaa ttctgcaaca 960  
tctctgtccc aggacaatag gaaaaaaagaa caggatggtg gtgacccaa tgaagagact 1020  
ccaatgtaa 1029

<210> 32  
<211> 342  
<212> PRT  
<213> Homo sapiens

<400> 32

Met	Gln	Ala	Val	Asp	Asn	Leu	Thr	Ser	Ala	Pro	Gly	Asn	Thr	Ser	Leu
1				5					10					15	
Cys	Thr	Arg	Asp	Tyr	Lys	Ile	Thr	Gln	Val	Leu	Phe	Pro	Leu	Leu	Tyr
					20				25					30	
Thr	Val	Leu	Phe	Phe	Val	Gly	Leu	Ile	Thr	Asn	Gly	Leu	Ala	Met	Arg
					35				40					45	
Ile	Phe	Phe	Gln	Ile	Arg	Ser	Lys	Ser	Asn	Phe	Ile	Ile	Phe	Leu	Lys
					50			55			60				
Asn	Thr	Val	Ile	Ser	Asp	Leu	Leu	Met	Ile	Leu	Thr	Phe	Pro	Phe	Lys
					65			70			75			80	
Ile	Leu	Ser	Asp	Ala	Lys	Leu	Gly	Thr	Gly	Pro	Leu	Arg	Thr	Phe	Val
					85				90					95	
Cys	Gln	Val	Thr	Ser	Val	Ile	Phe	Tyr	Phe	Thr	Met	Tyr	Ile	Ser	Ile
					100			105			110				
Ser	Phe	Leu	Gly	Leu	Ile	Thr	Ile	Asp	Arg	Tyr	Gln	Lys	Thr	Thr	Arg
					115			120			125				
Pro	Phe	Lys	Thr	Ser	Asn	Pro	Lys	Asn	Leu	Leu	Gly	Ala	Lys	Ile	Leu
					130			135			140				
Ser	Val	Val	Ile	Trp	Ala	Phe	Met	Phe	Leu	Leu	Ser	Leu	Pro	Asn	Met
					145			150			155			160	

Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser  
                  165                     170                     175  
  
 Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr  
                  180                     185                     190  
  
 Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys  
                  195                     200                     205  
  
 Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg  
                  210                     215                     220  
  
 Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile  
                  225                     230                     235                     240  
  
 Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg  
                  245                     250                     255  
  
 Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala  
                  260                     265                     270  
  
 Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser  
                  275                     280                     285  
  
 Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser  
                  290                     295                     300  
  
 Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr  
                  305                     310                     315                     320  
  
 Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro  
                  325                     330                     335  
  
 Asn Glu Glu Thr Pro Met  
                  340

<210> 33  
 <211> 1077  
 <212> DNA  
 <213> Homo sapiens

<400> 33  
 atgtcggtct gctaccgtcc cccagggAAC gagacactgc tgagctggaa gacttcgccc 60  
 gccacaggca cagccttcct gctgctggcg gcgctgtgg ggctgcctgg caacggcttc 120  
 gtggtgtggc gcttggcgccc ctggcggcct gcacgggggc gaccgctggc ggccacgctt 180  
 gtgctgcacc tggcgctggc cgacggcgcc gtgctgtgc tcacgcccgt ctttgtggcc 240

ttcctgaccc ggcaggcctg gccgtggc caggcggct gcaaggcggt gtactacgtg 300  
tgcgcgctca gcatgtacgc cagcgtctg ctcaccggcc tgctcagcct gcagcgctgc 360  
ctcgcagtca cccgcccctt cctggcgctt cggctgcga gcccggccct ggcccgccgc 420  
ctgctgctgg cggtctggct ggccggccctg ttgctcgccg tcccggccgc cgtctaccgc 480  
cacctgtgga gggaccgcgt atgccagctg tgccacccgt cgccggctca cgccggccgc 540  
cacctgagcc tggagactct gaccgcttc gtgcttcctt tcgggctgat gctcggctgc 600  
tacagcgtga cgctggcacf gctgcgggac gcccgtggg gctccgggac gcacggggac 660  
cggtgggac ggctggtag cgccatcgta cttgccttcg gcttgcctcg ggccccctac 720  
cacgcagtca accttctgca ggcggtcgca ggcgtggctc caccgaaagg ggccttggcg 780  
aagctggcg gagccggcca ggcggcgca gcgggaacta cggccttggc cttttcagt 840  
tctagcgtca acccggtgt ctacgtctc accgctggag atctgctgcc ccggcaggt 900  
ccccgtttcc tcacgcggct cttcgaaggc tctggggagg cccgaggggg cggccgctct 960  
agggaaaggga ccatggagct ccgaactacc cctcagctga aagtgggtggg gcagggccgc 1020  
ggcaatggag acccggggggg tggatggag aaggacggc cggaaatggga cctttga 1077

<210> 34  
<211> 358  
<212> PRT  
<213> Homo sapiens

<400> 34  
Met Ser Val Cys Tyr Arg Pro Pro Gly Asn Glu Thr Leu Leu Ser Trp  
1 5 10 15  
  
Lys Thr Ser Arg Ala Thr Gly Thr Ala Phe Leu Leu Ala Ala Leu  
20 25 30  
  
Leu Gly Leu Pro Gly Asn Gly Phe Val Val Trp Ser Leu Ala Gly Trp  
35 40 45  
  
Arg Pro Ala Arg Gly Arg Pro Leu Ala Ala Thr Leu Val Leu His Leu  
50 55 60  
  
Ala Leu Ala Asp Gly Ala Val Leu Leu Thr Pro Leu Phe Val Ala  
65 70 75 80  
  
Phe Leu Thr Arg Gln Ala Trp Pro Leu Gly Gln Ala Gly Cys Lys Ala  
85 90 95  
  
Val Tyr Tyr Val Cys Ala Leu Ser Met Tyr Ala Ser Val Leu Leu Thr  
100 105 110  
  
Gly Leu Leu Ser Leu Gln Arg Cys Leu Ala Val Thr Arg Pro Phe Leu  
115 120 125  
  
Ala Pro Arg Leu Arg Ser Pro Ala Leu Ala Arg Arg Leu Leu Leu Ala  
130 135 140

Val Trp Leu Ala Ala Leu Leu Leu Ala Val Pro Ala Ala Val Tyr Arg  
145 150 155 160

His Leu Trp Arg Asp Arg Val Cys Gln Leu Cys His Pro Ser Pro Val  
165 170 175

His Ala Ala Ala His Leu Ser Leu Glu Thr Leu Thr Ala Phe Val Leu  
180 185 190

Pro Phe Gly Leu Met Leu Gly Cys Tyr Ser Val Thr Leu Ala Arg Leu  
195 200 205

Arg Gly Ala Arg Trp Gly Ser Gly Arg His Gly Ala Arg Val Gly Arg  
210 215 220

Leu Val Ser Ala Ile Val Leu Ala Phe Gly Leu Leu Trp Ala Pro Tyr  
225 230 235 240

His Ala Val Asn Leu Leu Gln Ala Val Ala Ala Leu Ala Pro Pro Glu  
245 250 255

Gly Ala Leu Ala Lys Leu Gly Gly Ala Gly Gln Ala Ala Arg Ala Gly  
260 265 270

Thr Thr Ala Leu Ala Phe Phe Ser Ser Ser Val Asn Pro Val Leu Tyr  
275 280 285

Val Phe Thr Ala Gly Asp Leu Leu Pro Arg Ala Gly Pro Arg Phe Leu  
290 295 300

Thr Arg Leu Phe Glu Gly Ser Gly Glu Ala Arg Gly Gly Arg Ser  
305 310 315 320

Arg Glu Gly Thr Met Glu Leu Arg Thr Thr Pro Gln Leu Lys Val Val  
325 330 335

Gly Gln Gly Arg Gly Asn Gly Asp Pro Gly Gly Met Glu Lys Asp  
340 345 350

Gly Pro Glu Trp Asp Leu  
355

<210> 35  
<211> 1005  
<212> DNA  
<213> Homo sapiens

<400> 35

atgctgggaa tcatggcatg gaatgcaact tgcaaaaact ggctggcagc agaggctgcc 60  
ctggaaaagt actacatttc catttttat gggattgagt tcgttgtgg agtccttgg 120  
aataccattt acctctctgt ctctgactta gctttctgt gcaccctccc catgctgata 180  
tatctcttta acctctctgt ctctgactta gctttctgt gcaccctccc catgctgata 240  
aggagttatg ccaatggaaa ctggatatat ggagacgtgc tctgcataag caaccgatat 300  
gtgcttcatg ccaacctcta taccagcatt ctcttctca cttttatcag catagatcga 360  
tacttgataa ttaagtatcc ttcccgagaa cacctctgc aaaagaaaaga gtttgctatt 420  
ttaatctcct tggccatttgc gttttagta accttagagt tactaccat acttccccctt 480  
ataaaatcctg ttataactga caatggcacc acctgtaatg attttgcaag ttctggagac 540  
cccaactaca acctcattta cagcatgtgt ctaacactgt tggggttcct tattccttctt 600  
tttgtatgt gtttctttta ttacaagatt gctctttcc taaagcagag gaataggcag 660  
gttgctactg ctctgcccct tgaaaagcct ctcaacttgg tcatcatggc agtggtaatc 720  
ttctctgtgc tttttacacc ctatcacgtc atgcggaatg tgaggatcgc ttacgcctg 780  
gggagttgga agcagtatca gtgcactca gtcgtcatca actcccttta catttgac 840  
cggcctttgg cctttctgaa cagtgtcatc aaccctgtct tctatttct tttgggagat 900  
cacttcaggg acatgctgat gaatcaactg agacacaact tcaaattccct tacatccttt 960  
agcagatggg ctcatgaact cctactttca ttccagagaaa agtga 1005

<210> 36

<211> 334

<212> PRT

<213> Homo sapiens

<400> 36

Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala  
1 5 10 15

Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile  
20 25 30

Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr  
35 40 45

Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn  
50 55 60

Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile  
65 70 75 80

Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile  
85 90 95

Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe  
100 105 110

Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe  
                  115                 120                 125  
  
 Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu  
                  130                 135                 140  
  
 Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu  
                  145                 150                 155                 160  
  
 Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala  
                  165                 170                 175  
  
 Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr  
                  180                 185                 190  
  
 Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr  
                  195                 200                 205  
  
 Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala  
                  210                 215                 220  
  
 Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile  
                  225                 230                 235                 240  
  
 Phe Ser Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile  
                  245                 250                 255  
  
 Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val  
                  260                 265                 270  
  
 Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser  
                  275                 280                 285  
  
 Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp  
                  290                 295                 300  
  
 Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe  
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 Ser Arg Trp Ala His Glu Leu Leu Ser Phe Arg Glu Lys  
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gtgccatttg tccagtctac cgctgttgt acagaaaatgc tcactatgac ctgcattgct 420  
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Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg  
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Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu  
35 40 45

Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala  
50 55 60

Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr  
65 70 75 80

Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe  
85 90 95

Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu  
100 105 110

Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala  
115 120 125

Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His  
130 135 140

Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg  
145 150 155 160

Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val  
165 170 175

Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe  
180 185 190

Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro  
195 200 205

Val His Gln Lys Ile Tyr Thr Phe Ile Leu Val Ile Leu Phe Leu  
210 215 220

Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu  
225 230 235 240

Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile  
245 250 255

His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Arg Ala Val  
260 265 270

Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro  
275 280 285

Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu  
290 295 300

Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile  
305 310 315 320

Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn  
325 330 335

Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val  
340 345 350

Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr  
355 360 365

Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu  
370 375 380

Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu  
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aagagtggac cagccctgtg caccagaaga tctacaccac cttcatcctt gtcatacctct 180  
tcctcctgcc tcttatggtg atgcttattc tgtacgtaaa attggttatg aactttggat 240  
aaagaaaaga gttggggatg gttcagtgtc tcgaactatt catggaaaag aaatgtccaa 300  
aatagccagg aagaagaaaac gagctgtcat tatgatggtg acagtggtgg ctctcttgc 360  
tgtgtgctgg gcaccattcc atgttgtcca tatgatgatt gaatacagta atttgaaaa 420  
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26

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